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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 04:55:04 ; Search time 400 Seconds
(without alignments)
1858.587 Million cell updates/sec

Title: US-09-808-388-5_COPY_1_175

Perfect score: 175

Sequence: 1 cgcggcaaaactgctgctgaaa.....tccccagccttgctgctcact 175

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_29Jan04.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002s.*

7: geneseqn2003as.*

8: geneseqn2003bs.*

9: geneseqn2003cs.*

10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	175	100.0	271	4	AAI64307	Partial h
2	175	100.0	332	4	AAI64308	Partial s
3	171.4	97.9	1116	2	AAZ41274	Human nor
4	171.4	97.9	6172	1	AAAN91825	HindIII f
5	128	73.1	1080	1	AAAN91259	Nucleotid
6	128	73.1	1080	7	ACC46920	Human pho
7	110.8	63.3	5356	6	ABL70442	Chemical
8	110.8	63.3	5728	6	ABK31473	Signal tr
9	110.8	63.3	6083	4	AAAS46715	Tumour su
10	94.8	54.2	5356	6	ABL70441	Chemical
11	94.8	54.2	5728	6	ABK31472	Signal tr
12	94.8	54.2	6083	4	AAAS46714	Tumour su
13	47	26.9	3330	6	ABK63588	Rat sequ
14	47	26.9	3330	7	ABT42455	Toxicity
15	47	26.9	3330	9	ADB59181	Toxicity
16	44.4	25.4	4990	7	ACC47000	Mouse pho
17	31.2	17.8	420	3	AAAC61755	CDNA enco
18	31.2	17.8	1441	3	AAAC61753	CDNA enco
19	31.2	17.8	2236	3	AAAC61749	CDNA enco
20	31.2	17.8	2307	6	ABZ11921	Human pol
21	31.2	17.8	2604	3	AAAC61758	CDNA enco
22	31.2	17.8	2701	3	AAAC61747	CDNA enco
23	31.2	17.8	3320	6	ABA05868	Human lip

24	31.2	17.8	3320	9	AAD60556	Human lip
25	31.2	17.8	3384	3	AAC61761	CDNA enco
26	30.8	17.6	2368	4	AAAS41588	CDNA enco
27	30.8	17.6	2735	4	AAAS41048	CDNA enco
28	30.6	17.5	305	3	AAZ80534	Human col
29	30.6	17.5	2433	2	AAT29396	Apoptosis
30	30.6	17.5	2856	6	ABK92173	Prostate
31	30.6	17.5	2856	9	ACF79927	Breast ca
32	30.6	17.5	2885	6	ABN96891	Gene #338
33	30.6	17.5	2885	7	ACA56545	Human sig
34	30.6	17.5	2885	7	ADA05885	Human NOV
35	30.6	17.5	3370	7	ABX63339	Human cDN
36	30.4	17.4	1549	2	AAZ22842	Human zln
37	30.4	17.4	2835	9	ADB63347	Human cDN
38	30.2	17.3	499	8	ACH33946	Human end
39	30.2	17.3	669	4	AAAS30751	Human cDN
40	30.2	17.3	1004	4	AAAS33189	DNA encod
41	30.2	17.3	1022	4	AAAS33069	DNA encod
42	30.2	17.3	1038	4	AAAS33340	DNA encod
43	30.2	17.3	1082	6	ABQ55033	Human ova
44	30.2	17.3	1190	4	AAAS33153	DNA encod
45	30.2	17.3	1227	4	AAAS33320	DNA encod

ALIGNMENTS

RESULT 1

AAI64307

ID AAI64307 standard; DNA; 271 BP.

XX

AC AAI64307;

XX

DT 15-NOV-2001 (first entry)

XX

DE Partial human PLA2SIIA gene promoter.

XX

KW PPAR response element; antiinflammatory; antiarthritic; cytostatic;

KW cardiant; nootropic; promoter; arthritis; tumour; PLA2SIIA;

KW peroxisome proliferator activated receptor; human;

KW secreted non-pancreatic phospholipase A2; ds.

XX

OS Homo sapiens.

XX

FN WO200168845-A2.

XX

PD 20-SEP-2001.

XX

PF 14-MAR-2001; 2001WO-FR000759.

XX

PR 14-MAR-2000; 2000FR-00003262.

XX

PA 13-APR-2000; 2000US-0196959P.

XX

PI (AVET) AVENTIS PHARMA SA.

XX

PT Massaad C, Berenbaum F, Olivier J, Salvat C, Bereziat G;

XX

PS WPI; 2001-582451/65.

XX

PT New hybrid promoter induced by inflammation, useful in gene therapy of

PT arthritis, comprises peroxisome proliferator activated receptor response

XX

PS Claim 5; Page 51; 52pp; French.

XX

CC The present invention relates to a hybrid promoter comprising (i) a PPAR

CC (peroxisome proliferator activated receptor) response element (PPRE); and

CC (ii) at least part of the promoter of the PLA2SIIA (secreted non-

CC pancreatic phospholipase A2) gene. The hybrid promoter can be used to

CC regulate expression of therapeutic transgenes for experimental,

CC clinical, therapeutic or diagnostic use, especially in chondrocytes for

CC treatment of arthritis, but also in bone, muscle, liver, heart, the

CC nervous system and tumours. The present sequence is a partial human

09/808,388
EXAMINER'S SEARCH NOTES
9/24/2004

CC PLA2sIIA promoter sequence, which was used to generate the hybrid
 CC promoter of the present invention
 XX
 SQ Sequence 271 BP; 70 A; 79 C; 71 G; 51 T; 0 U; 0 Other;
 Query Match 100.0%; Score 175; DB 4; Length 271;
 Best Local Similarity 100.0%; Pred. No. 6.4e-50;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
 Db 1 CGCGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
 QY 61 TCCTCAACTCTCTCTGCGCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGG 120
 Db 61 TCCTCAACTCTCTCTGCGCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGG 120
 QY 121 CGACCAATCTGAGTCCCAACTGACACGCGCCATCCCGAGCTTGTGCTCAC 175
 Db 121 CGACCAATCTGAGTCCCAACTGACACGCGCCATCCCGAGCTTGTGCTCAC 175

RESULT 2
 AA164308
 ID AA164308 standard; DNA; 332 BP.
 XX
 AC AA164308;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Partial synthetic PLA2sIIA gene promoter.
 XX
 KW PPAR response element; antiinflammatory; antiarthritic; cytostatic;
 KW cardiant; nootropic; promoter; arthritis; tumour; PLA2sIIA;
 KW peroxisome proliferator activated receptor;
 KW secreted non-pancreatic phospholipase A2; ds.
 XX
 OS Synthetic.
 XX
 XX WO200168845-A2.
 XX
 XX 20-SEP-2001.
 XX
 XX 14-MAR-2001; 2001WO-FR000759.
 XX
 XX 14-MAR-2000; 2000FR-00003262.
 PR
 PR 13-APR-2000; 2000US-0196959P.
 XX
 XX (AVET) AVENTIS PHARMA SA.
 PA

Massaad C, Berenbaum F, Olivier J, Salvat C, Bereziat G;
 WPI; 2001-582451/65.
 XX
 XX New hybrid promoter induced by inflammation, useful in gene therapy of
 PT arthritis, comprises peroxisome proliferator activated receptor response
 PT element and promoter of secreted phospholipase A2.
 XX
 XX Disclosure; Page 51-52; 52pp; French.
 XX
 XX The present invention relates to a hybrid promoter comprising (i) a PPAR
 CC (peroxisome proliferator activated receptor) response element (PPRE); and
 CC (ii) at least part of the promoter of the PLA2sIIA (secreted non-
 CC pancreatic phospholipase A2) gene. The hybrid promoter can be used to
 CC regulate expression of therapeutic transgenes, for experimental,
 CC clinical, therapeutic or diagnostic use, especially in chondrocytes for
 CC treatment of arthritis, but also in bone, muscle, liver, heart, the
 CC nervous system and tumours. The present sequence is a partial synthetic
 CC PLA2sIIA promoter sequence, which was used to generate the hybrid
 CC promoter of the present invention
 XX
 SQ Sequence 332 BP; 96 A; 91 C; 82 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 175; DB 4; Length 332;
 Best Local Similarity 100.0%; Pred. No. 6.9e-50;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
 Db 62 CGCGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 121
 QY 61 TCCTCAACTCTCTCTGCGCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGG 120
 Db 122 TCCTCAACTCTCTCTGCGCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGG 181
 QY 121 CGACCAATCTGAGTCCCAACTGACACGCGCCATCCCGAGCTTGTGCTCAC 175
 Db 182 CGACCAATCTGAGTCCCAACTGACACGCGCCATCCCGAGCTTGTGCTCAC 236

RESULT 3
 AA241274
 ID AA241274 standard; cDNA; 1116 BP.
 XX
 AC AA241274;
 XX
 DT 18-JAN-2000 (first entry)
 XX
 DE Human normal ovarian tissue derived cDNA 53.
 DE
 XX Human; ovary; screening; ovarian cancer; treatment; ss.
 KW
 KW Homo sapiens.
 OS
 XX DE19816395-A1.
 PN
 XX 07-OCT-1999.
 PD
 XX 03-APR-1998; 98DE-01016395.
 PF
 XX 03-APR-1998; 98DE-01016395.
 PR
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 PA
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl B;
 PI
 PI WPI; 1999-552352/47.
 XX
 XX Nucleic acid sequences potentially useful in diagnosis or therapy of
 PT ovarian cancer.
 PT
 XX
 XX Claim 3; Page 164; 274pp; German.
 PS
 XX This invention describes novel nucleic acid sequences that are highly
 CC expressed in normal ovary tissue. Artificial chromosomes and cosmid
 CC clones containing the sequences can be used as gene transfer vehicles.
 CC The sequences can be used to produce DNA fragments containing full-length
 CC genes. Host cells transformed with the sequences can be used to produce
 CC polypeptides or polypeptide fragments, which can be used to screen phage
 CC displays for polypeptides that bind to them, or as tools for identifying
 CC agents active against ovarian cancer, or to prepare medicaments for
 CC treating ovarian cancer. The cDNA sequences can be used to obtain genomic
 CC structures and their promoters, enhancers, silencers, exon structures, intron
 CC structures and their splice variants. AA241222-241324 represent cDNA
 CC sequences derived from normal human ovarian tissue and which encode the
 CC protein fragments represented in AA259724-V59837
 XX
 SQ Sequence 1116 BP; 311 A; 311 C; 266 G; 228 T; 0 U; 0 Other;
 Query Match 97.9%; Score 171.4; DB 2; Length 1116;
 Best Local Similarity 99.4%; Pred. No. 1.8e-48;
 Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 CGCGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 62
 Db 6 CTGCAAAACCTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 65

CC contains 5 copies of the X chromosome (GMS009). The plaques were screened
CC for a gene encoding PRA2 using probes designed from peptides derived from
CC the purified protein. A positive clone, PRA2 8.5 EMBL3 was purified and a
CC 6.2 kb insert sequenced (shown here). Corresponding cDNA sequences (i.e.
CC without introns; see N97209) can be ligated into expression vectors for
CC the prodn. of recombinant PRA2. The protein, and antibodies raised to it,
CC can be used for diagnosis of inflammation and tissue injury associated
CC with various diseases. See also N91826-33 and N97209. (Updated on 25-MAR-
CC 2003 to correct PR field.)
XX
SQ Sequence 6172 BP; 1624 A; 1408 C; 1740 G; 1400 T; 0 U; 0 Other;

63	CTCAACTCTGTCTGCGCACTGATCAGGGGAAGAAAGGATTACCTAGGGGTATGGCG	122
QY		
66	CTCAACTCTGTCTGCGCACTGATCAGGGGAGAAAGGATTACCTAGGGGTATGGCG	125
Db		
123	ACCAATCTGTAGTCACCAACTGACCGCCATCCCGAGCCTTGTGCCTCAC	175
QY		
126	ACCAATCTGTAGTCACCAACTGACCGCCATCCCGAGCCTTGTGCCTCAC	178
Db		

SQ	Sequence	6172 BP;	1624 A;	1408 C;	1740 G;	1400 T;	0 U;	0 Other;
	Query Match	37.9%;	Score	171.4;	DB	1;	Length	6172;
	Best Local Similarity	59.4%;	Pred. No.	3.4e-48;				
	Matches	172;	Conservative	0;	Mismatches	1;	Indels	0;
	Gaps	0;						
Qy	3	CGGCAAACTGCTGAAATGTTGTTGGCATCAGCTACTCACACGTAAGGTTTCCCAATC	62					
Db	1378	CTGCAAACTGCTGAAATGTTGTTGGCATCAGCTACTCACACGTAAGGTTTCCCAATC	1437					
Qy	63	CTCAACTCTCTCTCGCCAGCTGATGAGGGGCAAGGAAAGGATTAACCTAGGGGTATGGGCG	122					
Db	1438	CTCAACTCTCTCTCGCCAGCTGATGAGGGGCAAGGAAAGGATTAACCTAGGGGTATGGGCG	1497					
Qy	123	ACCAATCTGAGTCCACAACTGACCACGCCCATCCCGACCTTGTGCGCTCAC	175					
Db	1498	ACCAATCTGAGTCCACAACTGACCACGCCCATCCCGACCTTGTGCGCTCAC	1550					

RESULT 4
AAN91825
ID AAN91825 standard; DNA; 6172 BP.
XX
XX AAN91825;
AC AC
XX
XX 25-MAR-2003 (revised)
DT DT
DT 31-JUL-1992 (first entry)
XX
XX
DE HindIII fragment of PLA2 8.5 EMBL3 encoding human inflammatory
DE phospholipase A2.
DE
XX
XX
XX Inflammation; acid stable; phosphatide 2-acylhydrolase; lipolytic;
KW glycerophospholipids; non-pancreatic; ss.
KW

Db	1498	ACCAATCTGAGTCCCAACTGACCAAGCCCATCCCCAGCCTTGCGCTCAC	1550
RESULT 5			
	AAN91259		
ID	AAN91259	standard; DNA; 1080 BP.	
XX			
XX	AAN91259;		
AC			
XX			
XX			
25-MAR-2003	(revised)		
DT			
27-JUN-1980	(first entry)		
DT			

OS	Homo sapiens.	Key	Location/Qualifiers
XX	exon	1..2492	
FT		/*tag= a	
FT		/number= 1	
FT	sig_peptide	2453..2721	
FT		/*tag= e	
FT	exon	2702..2846	
FT		/*tag= b	
FT		/number= 2	
FT	misc_feature	2715..2826	
FT		/*tag= g	
FT		/note= "Claim 24"	
FT	misc_feature	2715..2826	
FT		/*tag= g	
FT		/note= "Claim 24"	
FT	exon	3105..3211	
FT		/*tag= c	
FT		/number= 3	
FT	exon	5383..6172	
FT		/*tag= d	
FT		/number= 4	
FT	polyA_signal	5771..5776	
FT		/*tag= f	

XX	DE	Nucleotide sequence of exon 1 from genomic clone lambda sPLA2-6 of human
XX	DE	synovial phospholipase 2 (sPLA2) type A.
XX	XX	
XX	KW	Human synovial phospholipase A2 gene; clone lambda sPLA2-6; exon 1.
XX	XX	
XX	OS	Homo sapiens.
XX	XX	
XX	PH	Key
FT	FT	CAAT_signal
FT	FT	Location/Qualifiers
FT	FT	889..893
FT	FT	/*tag= a
FT	FT	968..974
FT	FT	/*tag= b
FT	FT	1016..1035
FT	FT	/*tag= c
FT	FT	/*note= "Exon 1"

FT		/tag= g	
FT		/note= "Claim 24"	
FT	misc_feature	2715..2826	
FT		/tag= g	
FT		/note= "Claim 24"	
FT	exon	3105..3211	
FT		/tag= c	
FT		/number= 3	
FT	exon	5383..6172	
FT		/tag= d	
FT		/number= 4	
FT	polyA_signal	5771..5776	
FT		/tag= f	
XX			
XX	WO8909818-A.		
PN			
XX			
PD	19-OCT-1989.		
XX			
PF	11-APR-1989;	89WO-US001418.	
XX			
PR	15-APR-1988;	88US-00181893.	
PR	12-JUL-1988;	88US-00219491.	
PA	(BIOJ) BIOGEN INC.		
XX			
PI	Kramer RM, Pepinsky R, Hession C;		
XX			
DR	WFI; 1989-324225/44.		
DR	P-PSDB; AAP93112.		
XX			
PT	Acid stable phospholipase A2 - used for prodn. of antibodies and in the treatment or diagnosis of inflammation and other diseases.		
XX			
PS	Claim 27; Fig 12; 84pp; English.		
XX			
CC	A genomic DNA library was prepd. from a mutant fibroblast cell line which		

XX Mammalian synovial phospholipase A2 - used in food processing, design and
PT screening of inflammation inhibitors, as an anticancer drug or vaccine
PT

PT adjuvant etc.

XX Fig 7; Page ?; 70pp; English.

XX EMBL3-human leucocyte genomic library was screened using labelled probes

CC (n90885 and n90887) based on sPLA2. Clone lambda SPLA2-6 is one of the

CC two unique sPLA2 clones thus identified. SPLA2-6 exons were identified

CC using the cDNA sequence in lambda sPLA2cDNA-4 (n91258). There are five

CC exons in lambda SPLA-6. This is the first one. The other four are in

CC n91260. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-

CC 2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 1080 BP; 306 A; 242 C; 303 G; 229 T; 0 U; 0 Other;

Query Match 73.1%; Score 128; DB 1; Length 1080;

Best Local Similarity 89.9%; Pred. No. 1.5e-33;

Matches 160; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

QY 1 CGCGGCAAAACTGCCTGAAATGTTTGGCATCAGCTACTGACACGTAAG-GGTTTCCCA 59

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

763 CTCGGCAAAACTGCCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCA 822

QY 60 ATCTCTCAACTCTGTCTCTG--CCAGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTAT 117

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

823 ATCTCTCAACTCTGTCTGCGCAGGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTAT 882

QY 118 GGGCGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCCTCAC 175

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

883 GGGCGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCCTCAC 940

RESULT 6

ABL70442/c

ID ABL70442 standard; DNA; 1080 BP.

XX

AC ACC46920;

XX

DT 05-JUN-2003 (first entry)

XX

DE Human phospholipase A2 group IIA (synovial) nucleotide sequence SEQ.17.

XX

KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;

KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;

KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;

KW psoriasis; diabetes; enzyme; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200297133-A1.

XX

PD 05-DEC-2002.

XX

PF 21-MAY-2002; 2002WO-US016135.

XX

PR 25-MAY-2001; 2001US-00865866.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Bennett CF, Wyatt JR;

XX

DR WPI; 2003-140495/13.

XX

PT New compound that hybridizes with and inhibits the expression of

PT Phospholipase A2, group IIA, useful for preparing a composition for

PT treating or preventing inflammation, cancer, psoriasis or diabetes.

XX

PS Example 15; Page 99-100; 135pp; English.

XX

CC The present invention describes a compound (I) comprising 8-50

CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,

CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase

CC A2, group IIA (synovial), where the compound specifically hybridises with

CC and inhibits the expression of phospholipase A2, group IIA (synovial).

CC

CC Also described: (1) a composition comprising the compound and a carrier

CC or diluent; (2) a method of inhibiting the expression of phospholipase

CC A2, group IIA in cells or tissues; and (3) a method of treating an animal

CC having a disease or condition associated with phospholipase A2, group IIA

CC (synovial). (1) has antiinflammatory, antidiabetic, cytostatic and

CC antipsoriatic activities, and can be used in vaccines and in gene

CC therapy. The compound (I) can be used for preparing a composition for

CC treating or preventing inflammation, cancer, psoriasis or diabetes. The

CC present sequence represents a human phospholipase A2 group IIA (synovial)

CC nucleotide sequence, which is used in an example from the present

CC invention

XX

SQ Sequence 1080 BP; 306 A; 242 C; 303 G; 229 T; 0 U; 0 Other;

Query Match 73.1%; Score 128; DB 7; Length 1080;

Best Local Similarity 89.9%; Pred. No. 1.5e-33;

Matches 160; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

QY 1 CGCGGCAAAACTGCCTGAAATGTTTGGCATCAGCTACTGACACGTAAG-GGTTTCCCA 59

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

763 CTCGGCAAAACTGCCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCA 822

QY 60 ATCTCTCAACTCTGTCTCTG--CCAGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTAT 117

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

823 ATCTCTCAACTCTGTCTGCGCAGGCTGATGAGGGGAAGAAAGGGATTACCTAGGGGTAT 882

QY 118 GGGCGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCCTCAC 175

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

883 GGGCGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCCTCAC 940

RESULT 7

ABL70442/c

ID ABL70442 standard; DNA; 5356 BP.

XX

AC ABL70442;

XX

DT 01-JUL-2002 (first entry)

XX

DE Chemically treated cell signalling DNA sequence complementary to#166.

XX

KW Cell signalling; cytosine methylation; cell signalling disease; cancer;

KW tumour; cytostatic; ds.

XX

OS Unidentified.

XX

PN WO200202807-A2.

XX

PD 10-JAN-2002.

XX

PF 29-JUN-2001; 2001WO-EP007471.

XX

PR 30-JUN-2000; 2000DE-01032529.

XX

PR 01-SEP-2000; 2000DE-01043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2002-154758/20.

XX

PT Nucleic acid, useful for diagnosis and therapy of diseases associated

PT with cell signalling e.g. cancer, comprises chemically modified genomic

PT sequences of genes associated with cell signalling.

XX

PS Claim 1; SEQ ID NO 332; 24pp + Sequence Listing; English.

XX

CC The invention relates to a nucleic acid comprising a sequence of at least

CC 18 bases of a segment of chemically pretreated DNA of genes associated

CC with cell signalling. The activity of the modified sequences of the

CC invention may be described as cytostatic. The object of the invention is

CC to provide the chemically modified DNA of genes associated with cell

CC signalling, as well as oligonucleotides and/or PNA-oligomers for

CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnosis
CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL70111-ABL70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling. Note: The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office
XX
SQ Sequence 5356 BP; 1357 A; 60 C; 1167 G; 2772 T; 0 U; 0 Other;

Query Match 63.3%; Score 110.8; DB 6; Length 5356;
Best Local Similarity 78.2%; Pred. No. 2.2e-27;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 CAAAACTGCTGAAATGTGTTTGGCATCAGTACTGACACGTAAGTTCCTCAATCCTC 65
DB 1324 CAAAACTGCTGAAATGTGTTTGGCATCAGTACTGACACGTAAGTTCCTCAATCCTC 1265
QY 66 AACTCTGTCTGCTGCACTGATGAGGGGAGGAAAGGATTAACCTAGGGGTATGGCGACC 125
DB 1264 AACTCTATCTCTACCAACTAATAAAAAAATAAAAAATTAACCTAAAAATATAACGACC 1205
QY 126 AATCTGTAGTCCACCACTGACACGCGCATCCCGAGCTTGTGCTCTAC 175
DB 1204 AATCTCTAAATCCCACTAACCACGCGCATCCCGAGCTTATACCTCTAC 1155

RESULT 8
ABK31473/c
ID ABK31473 standard; DNA; 5728 BP.
XX
AC ABK31473;
XX
DT 23-APR-2002 (first entry)
XX
DE Signal transduction associated gene modified complementary DNA #158.

XX Human; signal transduction associated gene; cytosine methylation state;
KW CpG island; signal transduction associated disease; solid tumour; cancer;
KW antitumour; cytostatic; mutant; ds.
XX

OS Homo sapiens.
OS Synthetic.

XX WO200200926-A2.

XX 03-JAN-2002.

XX 29-JUN-2001; 2001WO-EP007472.

XX 30-JUN-2000; 2000DE-01032529.

XX 01-SEP-2000; 2000DE-01043826.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-147896/19.

XX Oligonucleotide for diagnosis and therapy of diseases associated with
PT signal transduction e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with signal transduction.

PS Claim 1; SEQ ID NO 316; 24pp; English.

XX The present invention relates to chemically modified DNA sequences of
CC signal transduction associated genes. The DNA sequences are chemically
CC modified using a solution of bisulphite, hydrogen sulphite or disulphite.
CC Also disclosed are oligonucleotides and/or PNA oligomers for detecting
CC the cytosine methylation state (CpG islands) of these genes, and a method

CC for the diagnosis and/or therapy of genetic and epigenetic parameters of
CC genes associated with signal transduction. The genomic DNA can be
CC obtained from cells or cellular components which contain DNA, e.g. cell
CC lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid,
CC tissue embedded in paraffin such as tissue from eyes, intestine, kidney,
CC brain, heart, prostate, lung, breast or liver, histologic object slides,
CC and all their possible combinations. The sequences of the invention are
CC useful for the diagnosis and therapy of diseases associated with signal
CC transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent
CC chemically pretreated genomic DNA sequences of different genes associated
CC with signal transduction, or their complementary sequences. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office
XX

SQ Sequence 5728 BP; 1462 A; 79 C; 1271 G; 2916 T; 0 U; 0 Other;

Query Match 63.3%; Score 110.8; DB 6; Length 5728;
Best Local Similarity 78.2%; Pred. No. 2.3e-27;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 CAAAACTGCTGAAATGTGTTTGGCATCAGTACTGACACGTAAGTTCCTCAATCCTC 65
DB 969 CAAAACTGCTGAAATGTGTTTGGCATCAGTACTGACACGTAAGTTCCTCAATCCTC 910

QY 66 AACTCTGTCTGCTGCACTGATGAGGGGAGGAAAGGATTAACCTAGGGGTATGGCGACC 125
DB 909 AACTCTATCTCTACCAACTAATAAAAAAATAAAAAATTAACCTAAAAATATAACGACC 850

QY 126 AATCTGTAGTCCACCACTGACACGCGCATCCCGAGCTTGTGCTCTAC 175
DB 849 AATCTCTAAATCCCACTAACCACGCGCATCCCGAGCTTATACCTCTAC 800

RESULT 9
AAS46715/c
ID AAS46715 standard; DNA; 6083 BP.
XX
AC AAS46715;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #438.
XX Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
XX WO200168912-A2.
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-EP002955.
XX
XX 15-MAR-2000; 2000DE-01013847.
XX 06-APR-2000; 2000DE-01019058.
XX 07-APR-2000; 2000DE-01019173.
XX 30-JUN-2000; 2000DE-01032529.
XX 01-SEP-2000; 2000DE-01043826.
XX
XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-602752/68.

XX Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.

PS Claim 1; SEQ ID NO 438; 27pp; English.

XX The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisphosphate, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Sequences with even
CC numbered Seq ID numbers are the complementary sequence of the
CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
CC 535, except for those whose partner sequence is missing). Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 6083 BP; 1525 A; 83 C; 1367 G; 3108 T; 0 U; 0 Other;

Query Match 63.3%; Score 110.8; DB 4; Length 6083;
Best Local Similarity 78.2%; Pred. No. 2.3e-27;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 CAAACTGCTCCGCAATGTTGTTGGCATCAGTACTGACAGTAAAGTTTCCCAATCCTC 65
Db 1324 CAAAACTACCTAAAATATATTTTAACATCAACTACTAAACGTAATAATTTCCCAATCCTC 1265

QY 66 AACTCTGCTCCGCAATGTTGTTGGCATCAGTACTGACAGTAAAGTTTCCCAATCCTC 125
Db 1264 AACTCTATCTTACCACTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1205

QY 126 AATCTGAGTCCACCACTGACAGCCATCCCGCCTGCTGCTCAC 175
Db 1204 AATCTGAGTCCACCACTGACAGCCATCCCGCCTGCTGCTCAC 1155

RESULT 10
ABL70441
ID ABL70441 standard; DNA; 5356 BP.
XX
AC ABL70441;
XX
DT 01-JUL-2002 (first entry)
XX
DE Chemically treated cell signalling DNA sequence#166.
XX
KW Cell signalling; cytosine methylation; cell signalling disease; cancer;
KW tumour; cytostatic; ds.
XX
OS Unidentified.
XX
FN WO200202807-A2.
XX
PD 10-JAN-2002.
XX
PP 29-JUN-2001; 2001WO-EP007471.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX

DR WPI; 2002-154758/20.
XX
PT Nucleic acid, useful for diagnosis and therapy of diseases associated
PT with cell signalling e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with cell signaling.
XX
XX Claim 1; SEQ ID NO 331; 24pp + Sequence Listing; English.
PS
XX The invention relates to a nucleic acid comprising a sequence of at least
CC 18 bases of a segment of chemically pretreated DNA of genes associated
CC with cell signalling. The activity of the modified sequences of the
CC invention may be described as cytostatic. The object of the invention is
CC to provide the chemically modified DNA of genes associated with cell
CC signalling, as well as oligonucleotides and/or PNA-oligoners for
CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnosis
CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL70111-ABL70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling. Note: The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office
XX
SQ Sequence 5356 BP; 1476 A; 60 C; 1356 G; 2464 T; 0 U; 0 Other;

Query Match 54.2%; Score 94.8; DB 6; Length 5356;
Best Local Similarity 72.4%; Pred. No. 7e-22;
Matches 123; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 5 GCAAACTGCTGCAATGTTGTTGGCATCAGTACTGACAGTAAAGTTTCCCAATCCTC 64
Db 4032 GTAAATATGTTGAAATGTTGTTGGTATTAGTTATTGATACGTAAGGTTTTTAAATTTT 4091

QY 65 CAATCTGCTCCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGAC 124
Db 4092 TAAATTTGTTTGTAGTTGATGAGGGGAAGGAAGGATTATTAGGGGTATGGCGAT 4151

QY 125 CAATCTGAGTCCCACTGACCACTGACCACTGACCACTGACCACTGACCACTGACCACTGAC 174
Db 4152 TAAATTTGAGTTTAAATGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATT 4201

RESULT 11
ABK31472
ID ABK31472 standard; DNA; 5728 BP.
XX
AC ABK31472;
XX
DT 23-APR-2002 (first entry)
XX
DE Signal transduction associated gene modified DNA #158.
XX
KW Human; signal transduction associated gene; cytosine methylation state;
KW CpG island; signal transduction associated disease; solid tumour; cancer;
KW antitumour; cytostatic; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200200926-A2.
XX
PD 03-JAN-2002.
XX
PP 29-JUN-2001; 2001WO-EP007472.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;

```
XX WPI; 2002-147896/19.
DR
XX
XX Oligonucleotide for diagnosis and therapy of diseases associated with
PT signal transduction e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with signal transduction.
PT
XX Claim 1; SEQ ID NO 315; 24pp; English.
XX
XX The present invention relates to chemically modified DNA sequences of
CC signal transduction associated genes. The DNA sequences are chemically
CC modified using a solution of bisulphite, hydrogen sulphite or disulphite.
CC Also disclosed are oligonucleotides and/or PNA oligomers for detecting
CC the cytosine methylation state (CpG islands) of these genes, and a method
CC for the diagnosis and/or therapy of genetic and epigenetic parameters of
CC genes associated with signal transduction. The genomic DNA can be
CC obtained from cells or cellular components which contain DNA, e.g. cell
CC lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid,
CC tissue embedded in paraffin such as tissue from eyes, intestine, kidney,
CC brain, heart, prostate, lung, breast or liver, histologic object slides,
CC and all their possible combinations. The sequences of the invention are
CC useful for the diagnosis and therapy of diseases associated with signal
CC transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent
CC chemically pretreated genomic DNA sequences of different genes associated
CC with signal transduction, or their complementary sequences. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office
XX
XX Sequence 5728 BP; 1547 A; 79 C; 1448 G; 2654 T; 0 U; 0 Other;
XX
Query Match 54.2%; Score 94.8; DB 6; Length 5728;
Best Local Similarity 72.4%; Pred. No. 7.1e-22;
Matches 123; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 5 GCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCT 64
Db 4759 GTAATATTGTTGAATGTTTGGTATTAGTTATGATGATGATGTTTAAATTT 4818
QY 65 CAATCTGTCTCCAGCTGATGAGGGAAGGAAAGGATTACCTAGGGGTATGGCGAC 124
Db 4819 TAATTTGTTTGTAGTTGATGAGGGAAGGAAAGGATTATTAGGGGTATGGCGAT 4878
QY 125 CAATCTGTAGTCCCACTGACGACGCCCATCCCGAGCTTGTGCTCA 174
Db 4879 TAATTTGAGTTTAAATTAATTGATTAGTTTATTTTAGTTTGTGTTTA 4928
RESULT 12
ID AAS46714
XX AAS46714 standard; DNA; 6083 BP.
XX
XX AAS46714;
XX
XX 18-DEC-2001 (first entry)
XX
XX Tumour suppressor gene derived chemically modified sequence #437.
XX
XX Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
XX Homo sapiens.
XX
XX WO200168912-A2.
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-EP002955.
XX
XX 15-MAR-2000; 2000DE-01013847.
XX 06-APR-2000; 2000DE-01019058.
XX 07-APR-2000; 2000DE-01019173.
PR
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PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
XX (BPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-602752/58.
XX
XX Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.
XX
XX Claim 1; SEQ ID NO 437; 27pp; English.
XX
XX The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (SS) and sequences
CC complementary to (SS). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC fcp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 6083 BP; 1640 A; 83 C; 1551 G; 2809 T; 0 U; 0 Other;
XX
Query Match 54.2%; Score 94.8; DB 4; Length 6083;
Best Local Similarity 72.4%; Pred. No. 7.3e-22;
Matches 123; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 5 GCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCT 64
Db 4759 GTAATATTGTTGAATGTTTGGTATTAGTTATGATGATGATGTTTAAATTT 4818
QY 65 CAATCTGTCTCCAGCTGATGAGGGAAGGAAAGGATTACCTAGGGGTATGGCGAC 124
Db 4819 TAATTTGTTTGTAGTTGATGAGGGAAGGAAAGGATTATTAGGGGTATGGCGAT 4878
QY 125 CAATCTGTAGTCCCACTGACGACGCCCATCCCGAGCTTGTGCTCA 174
Db 4879 TAATTTGAGTTTAAATTAATTGATTAGTTTATTTTAGTTTGTGTTTA 4928
RESULT 13
ABK63588
ID ABK63588 standard; cDNA; 3330 BP.
XX
XX ABK63588;
XX
XX 18-JUN-2002 (first entry)
XX
XX Rat sequence differentially expressed in response to a hepatotoxin #1495.
XX
XX Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
KW differential expression; centrilobular necrosis; steatosis.
XX
XX Rattus norvegicus.
XX
XX WO200210453-A2.
XX
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PD 07-FEB-2002.

XX 30-JUL-2001; 2001WO-US023872.

XX 31-JUL-2000; 2000US-0222040P.

PR 02-NOV-2000; 2000US-0244880P.

PR 11-MAY-2001; 2001US-0290029P.

PR 15-MAY-2001; 2001US-0290645P.

PR 22-MAY-2001; 2001US-0292336P.

PR 06-JUN-2001; 2001US-0295798P.

PR 13-JUN-2001; 2001US-0297457P.

PR 19-JUN-2001; 2001US-0298884P.

PR 09-JUL-2001; 2001US-0303459P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;

XX WPI; 2002-241625/29.

XX Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.

XX Claim 1; SEQ ID NO 1495; 239pp; English.

XX The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilize a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information, identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent

XX Sequence 3330 BP; 858 A; 860 C; 958 G; 753 T; 0 U; 1 Other;

XX Query Match 26.9%; Score 47; DB 6; Length 3330;

XX Best Local Similarity 60.5%; Pred. No. 1.6e-05;

XX Matches 95; Conservative 0; Mismatches 60; Indels 2; Gaps 1;

QY 6 CAAACTCCTGAGTGTGTTGGATCAGTACGTACAGTAAGTTTCCCAATCTC 65

DB 260 CGAATCAGCTAAAGTTTATGATGCCCAACCCATGATGAGGGCTTTCCGGCCCTC 319

QY 66 AACTCTGCTCCAGCTGATGAGGGGAAGGAAGGATTAAGGAGGTATGGG--CGA 123

DB 320 AAGGCTGTTCGCCAGCTGTGGGGGAAAGGGGAATATCCAGGGCGTTGGTATGC 379

QY 124 CCAATCCTGAGTCCCAACTGACCAACGCCCATCCCC 160

Db 380 CCGTCTGTGAATCCATTTATTTGGCCACACCCACTCC 416

RESULT 14

ABT42455

ID ABT42455 standard; DNA; 3330 BP.

XX AC ABT42455;

XX 26-JUN-2003 (first entry)

XX Toxicity modelling related rat gene SEQ ID No 2157.

XX Toxic effect; gene expression profile; renal toxicity; toxicity marker; database; drug screening; toxicity assay; rat; ds.

XX Rattus norvegicus.

XX WO200295000-A2.

XX 28-NOV-2002.

XX 22-MAY-2002; 2002WO-US016173.

XX 22-MAY-2001; 2001US-0292335P.

PR 13-JUN-2001; 2001US-0297523P.

PR 19-JUN-2001; 2001US-0298925P.

PR 10-JUL-2001; 2001US-0303807P.

PR 10-JUL-2001; 2001US-0303808P.

PR 10-JUL-2001; 2001US-0303810P.

PR 28-AUG-2001; 2001US-0315047P.

PR 27-SEP-2001; 2001US-0324928P.

PR 22-OCT-2001; 2001US-0330462P.

PR 01-NOV-2001; 2001US-0330867P.

PR 21-NOV-2001; 2001US-0331805P.

PR 06-DEC-2001; 2001US-0336144P.

PR 19-DEC-2001; 2001US-0340873P.

PR 21-FEB-2002; 2002US-0357842P.

PR 21-FEB-2002; 2002US-0357843P.

PR 21-FEB-2002; 2002US-0357844P.

PR 15-MAR-2002; 2002US-0364134P.

PR 08-APR-2002; 2002US-0370144P.

PR 08-APR-2002; 2002US-0370206P.

PR 08-APR-2002; 2002US-0370247P.

PR 17-APR-2002; 2002US-0372794P.

PR 21-APR-2002; 2002US-0371679P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;

XX WPI; 2003-148464/14.

XX Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database.

XX Example 4; Page; 446pp; English.

XX The invention relates to a novel method of predicting at least one toxic effect of a compound. The method comprises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polynucleotide represents a rat DNA sequence relating to the toxic effect database

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 04:56:39 ; Search time 3552 Seconds
(without alignments)
2135.425 Million cell updates/sec

Title: US-09-808-388-5_COPY_1_175
Perfect score: 175
Sequence: 1 cggcgaaaactgcctgaaa.....tccccagcctgtgcctcac 175

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.em.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	175	100.0	271	6	AX251577	AX251577 Sequence
2	175	100.0	332	6	AX251578	AX251578 Sequence
3	171.4	97.9	1116	6	AX015387	AX015387 Sequence
4	171.4	97.9	1116	6	BD194533	BD194533 Human nuc
5	171.4	97.9	1268	6	AX015532	AX015532 Sequence
6	171.4	97.9	1268	6	BD194580	BD194580 Human nuc
7	171.4	97.9	8941	9	AY462114	AY462114 Homo sapi
8	171.4	97.9	101824	9	AL358253	AL358253 Human DNA
9	165	94.3	157470	2	AL360079	AL360079 Homo sapi
10	128	73.1	1080	6	I09231	I09231 Sequence 36
11	128	73.1	1080	9	HUMRASFA1	M22429 Human RASF-
12	110.8	63.3	5356	6	AX348874	AX348874 Sequence
13	110.8	63.3	5728	6	AX344469	AX344469 Sequence
14	110.8	63.3	6083	6	AX251472	AX251472 Sequence
15	94.8	54.2	5356	6	AX348873	AX348873 Sequence
16	94.8	54.2	5728	6	AX344468	AX344468 Sequence
17	94.8	54.2	6083	6	AX251471	AX251471 Sequence
18	47	26.9	2697	10	AF375595	AF375595 Rattus no
19	47	26.9	3330	6	AX401819	AX401819 Sequence
20	47	26.9	3330	10	RNPLA2G	X51529 Rat gene fo
21	47	26.9	150638	2	AC129994	AC129994 Rattus no
22	47	26.9	239739	2	AC116054	AC116054 Rattus no
23	47	26.9	282515	2	AC118094	AC118094 Rattus no
24	45.4	25.9	3366	10	RATGIIIPHOS	M37127 Rat group I
25	44.4	25.4	4438	10	MMU32313	U32313 Mus musculu
26	44.4	25.4	41125	10	AC002108	AC002108 Genomic s
27	44.4	25.4	186608	10	AL844178	AL844178 Mouse DNA
28	37.6	21.5	497	10	RNPHLPA2	X52613 Rat DNA for
29	34.4	19.7	201957	2	AC111113	AC111113 Mus muscu
30	33.4	19.1	194218	2	AC121770	AC121770 Mus muscu
31	32.4	18.5	1841	9	AK098681	AK098681 Homo sapi
32	32.4	18.5	99088	9	AC093401	AC093401 Homo sapi
33	32.4	18.5	119388	9	AC005866	AC005866 Homo sapi
34	32.4	18.5	158608	9	CNS05TDJ	AL358601 Human chr
35	32.4	18.5	256870	2	AC096904	AC096904 Rattus no
36	32.4	18.5	311677	2	AC118899	AC118899 Rattus no
37	32.2	18.4	123508	8	AC137620	AC137620 Oryza sat
38	32.2	18.4	150826	8	AC137928	AC137928 Oryza sat
39	32.2	18.4	160013	9	AL133325	AL133325 Human DNA
40	32.2	18.4	165867	2	AL353609	AL353609 Homo sapi
41	32.2	18.4	188439	2	EX678772	EX678772 Danio rer
42	32.2	18.4	171941	9	AL365274	AL365274 Human DNA
43	32.2	18.4	200395	9	AF274855	AF274855 Homo sapi
44	32	18.3	60945	9	AC079394	AC079394 Homo sapi
45	32	18.3	152319	9	AL137001	AL137001 Human DNA

ALIGNMENTS

RESULT 1	AX251577	Sequence 5 from Patent WO0168845.	271 bp	DNA	linear	PAT 05-OCT-2001
LOCUS	AX251577	Sequence 5 from Patent WO0168845.				
DEFINITION	AX251577	AX251577.1	GI:15985000			
ACCESSION	AX251577					
VERSION	AX251577.1					
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						

Massaad, C., Berenbaum, F., Olivier, J.L., Salvat, C. and Bereziat, G.
Inflammation-inducible hybrid promoters, vectors containing same
and uses thereof
Patent: WO 0168845-A 5 20-SEP-2001;

FEATURES
 Source
 Aventis Pharma S.A. (FR)
 Location/Qualifiers
 1..271
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 /db_xref="taxon:32630"
 /note="fragment du promoteur PLA2s"

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 Best Local Similarity 100.0%; Pred. No. 1.1e-48;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
 DB 1 CGCGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
 QY 61 TCCTCAACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGG 120
 DB 61 TCCTCAACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGG 120
 QY 121 CGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 175
 DB 121 CGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 175

RESULT 2
 LOCUS AX251578 332 bp DNA linear PAT 05-OCT-2001
 DEFINITION Sequence 6 from Patent WO0168845.
 ACCESSION AX251578
 VERSION AX251578.1 GI:15985001
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE
 AUTHORS Massaad,C., Berenbaum,F., Olivier,J.L., Salvat,C. and Bereziat,G.
 TITLE Inflammation-inducible hybrid promoters, vectors containing same
 and uses thereof
 JOURNAL Patent: WO 0168845-A 6 20-SEP-2001;
 Aventis Pharma S.A. (FR)

FEATURES
 source
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1.1e-48;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
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 QY 61 TCCTCAACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGG 120
 DB 122 TCCTCAACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGG 181
 QY 121 CGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 175
 DB 182 CGACCAATCCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 236

RESULT 3
 LOCUS AX015387 1116 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 53 from Patent WO9951727.
 ACCESSION AX015387
 VERSION AX015387.1 GI:10041367

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
 Pillarsky,C.
 TITLE Human nucleic acid sequences of normal ovary tissue
 JOURNAL Patent: WO 9951727-A 53 14-OCT-1999;
 SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
 BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
 (DE); PILLARSKY CHRISTIAN (DE)

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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

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 Best Local Similarity 99.4%; Pred. No. 2e-47;
 Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
 DB 6 CTGCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 65
 QY 63 CTCAACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCG 122
 DB 66 CTCAACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCG 125
 QY 123 ACCAATCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 175
 DB 126 ACCAATCTGAGTCCCACTGACACGCGCCATCCCGAGCTTGTGCTCTCAC 178

RESULT 4
 LOCUS BD194533 1116 bp DNA linear PAT 17-JUL-2003
 DEFINITION Human nucleic acid sequence originating in normal ovarian tissue.
 ACCESSION BD194533
 VERSION BD194533.1 GI:33004275
 KEYWORDS JP 2002510486-A/44.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Speft,T., Hintzman,B., Shcmitt,A., Pirarski,C., Duhl,E. and
 Rosenthal,A.
 TITLE Human nucleic acid sequence originating in normal ovarian tissue
 JOURNAL Patent: JP 2002510486-A 44 09-APR-2002;
 METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH

COMMENT
 OS Homo sapiens (human)
 ES JP 2002510486-A/44
 ED 09-APR-2002 JP 2000542440
 EF 31-MAR-1999 DE 198 16 395.9
 PR 03-APR-1998 DE 198 16 395.9
 PI THOMAS SPEFT,BERND HINTZMAN,ARMIN SHCMITT,CHRISTIAN PIRARSKI,
 EDGAR DUHL,
 PI ANDRE ROSENTHAL
 PC C12N15/09,A61K38/00,A61K48/00,A61P35/00,C07K14/47,C07K16/30,
 PC C12N1/15,
 PC C12N1/19,C12N1/21,C12N5/10,C12Q1/68,G01N33/574,C12N15/00, PC
 A61K37/02,
 PC C12N5/00
 CC Human nucleic acid sequence originating in normal ovarian CC
 tissue
 PH Key Location/Qualifiers
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 FT /organism='Homo sapiens (human)'.
 FT Location/Qualifiers

source 1. .1116
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Query Match 97.9%; Score 171.4; DB 6; Length 1116;
Best Local Similarity 99.4%; Pred. No. 2e-47;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGCAAAACGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
DB 6 CTGCAAAACGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 65

QY 63 CTCAACTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATACCTAGGGGTATGGCG 122
DB 66 CTCAACTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATACCTAGGGGTATGGCG 125

QY 123 ACCAATCTGAGTCCCACTGACACGAGCCCATCCCAAGCTTGTGCCTCAC 175
DB 126 ACCAATCTGAGTCCCACTGACACGAGCCCATCCCAAGCTTGTGCCTCAC 178

RESULT 5
AX015532/c

LOCUS AX015532 1268 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 226 from Patent WO9951727.
ACCESSION AX015532
VERSION AX015532.1 GI:10041414
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pilarsky,C.
Human nucleic acid sequences of normal ovary tissue
Patent: WO 9951727-A 226 14-OCT-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUNG
(DE); PILARSKY CHRISTIAN (DE)
Location/Qualifiers
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/db_xref="taxon:9606"

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Query Match 97.9%; Score 171.4; DB 6; Length 1268;
Best Local Similarity 99.4%; Pred. No. 2e-47;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 63 CTCAACTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATACCTAGGGGTATGGCG 122
DB 1203 CTCAACTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATACCTAGGGGTATGGCG 1144

QY 123 ACCAATCTGAGTCCCACTGACACGAGCCCATCCCAAGCTTGTGCCTCAC 175
DB 1143 ACCAATCTGAGTCCCACTGACACGAGCCCATCCCAAGCTTGTGCCTCAC 1091

RESULT 6
BD194580/c

LOCUS BD194580 1268 bp DNA linear PAT 17-JUL-2003
DEFINITION Human nucleic acid sequence originating in normal ovarian tissue.
ACCESSION BD194580
VERSION BD194580.1 GI:33004323
KEYWORDS
JP 2002510486-A/91.

source Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1268)
Specht,T., Hintzman,B., Schmitt,A., Pirarski,C., Duhl,E. and
Rosenthal,A.
Human nucleic acid sequence originating in normal ovarian tissue
Patent: JP 2002510486-A 91 09-APR-2002;
METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH
OS Homo sapiens (human)
PN JP 2002510486-A/91
PD 09-APR-2002
PF 31-MAR-1999 JP 2000542440
PR 03-APR-1998 DE 198 16 395.9
PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PIRARSKI,
PI EDGAR DUHL,
PI ANDRE ROSENTHAL
PC C12N15/09, A61K38/00, A61K48/00, A61P35/00, C07K14/47, C07K16/30,
PC C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12Q1/68, G01N33/574, C12N15/00, PC
A61K37/02,
PC C12N5/00
CC Human nucleic acid sequence originating in normal ovarian CC
tissue
FH Key Location/Qualifiers
FT source 1. .1268
/organism="Homo sapiens"
/mol_type="genomic DNA"
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FEATURES
source
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Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN

Query Match 97.9%; Score 171.4; DB 6; Length 1268;
Best Local Similarity 99.4%; Pred. No. 2e-47;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGCAAAACGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
DB 1263 CTGCAAAACGCTGAAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 1204

QY 63 CTCAACTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATACCTAGGGGTATGGCG 122
DB 1203 CTCAACTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATACCTAGGGGTATGGCG 1144

QY 123 ACCAATCTGAGTCCCACTGACACGAGCCCATCCCAAGCTTGTGCCTCAC 175
DB 1143 ACCAATCTGAGTCCCACTGACACGAGCCCATCCCAAGCTTGTGCCTCAC 1091

RESULT 7
AY462114

LOCUS AY462114 8941 bp DNA linear PRI 18-NOV-2003
DEFINITION Homo sapiens phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A) gene, complete cds.
ACCESSION AY462114
VERSION AY462114.1 GI:38304361
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 8941)
Livingston,R.J., Rieder,M.J., Chung,M.-W., Ritchie,T.K.,
Olson,A.N., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D.,
Schackwitz,W.S., Sherwood,G.K., Leithauser,B.J. and Nickerson,D.A.
Direct Submission
Submitted (10-NOV-2003) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: NIEHS-SNPs, Environmental Genome
Project NIEHS ES15478 Department of Genome Sciences, Seattle, WA

(URL: http://esp.gs.washington.edu).

FEATURES

source

Location/Qualifiers

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Best Local Similarity 99.4%; Pred. No. 2.2e-47;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATC 62
Db 2530 CTGCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATC 2589

QY 63 CTCAACTCTCTCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGCG 122
Db 2590 CTCAACTCTCTCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGCG 2649

QY 123 ACCAATCCTGAGTCCCAACTGACACGCCCATCCCGAGCTTGTGCCTCAC 175
Db 2650 ACCAATCCTGAGTCCCAACTGACACGCCCATCCCGAGCTTGTGCCTCAC 2702

RESULT 8
AL358253/c          101824 bp  DNA  linear  PRI 19-SEP-2002
LOCUS              Human DNA sequence from clone RP11-460G22 on chromosome 1, complete
DEFINITION
ACCESSION          AL358253
VERSION            AL358253.16 GI:23304623
KEYWORDS           HTG.
SOURCE             Homo sapiens (human)
ORGANISM           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE          1 (bases 1 to 101824)
AUTHORS            Bagguley,C.
TITLE              Direct Submission
JOURNAL            Submitted (19-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,
                  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                  humquerry@sanger.ac.uk
COMMENT            On Sep 23, 2002 this sequence version replaced gi:22797900.
                  ----- Genome Center
```

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e. phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl>
RP11-460G22 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6.

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Query Match 97.9%; Score 171.4; DB 9; Length 101824;
Best Local Similarity 99.4%; Pred. No. 2.4e-47;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 CGGCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATC 62
Db 73302 CTGCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATC 73243
QY 63 CTCAACTCTCTCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGCG 122
Db 73242 CTCAACTCTCTCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGCG 73183
QY 123 ACCAATCCTGAGTCCCAACTGACACGCCCATCCCGAGCTTGTGCCTCAC 175
Db 73182 ACCAATCCTGAGTCCCAACTGACACGCCCATCCCGAGCTTGTGCCTCAC 73130

RESULT 9

AL360079/c 157470 bp DNA linear HTG 10-JUL-2001
LOCUS Homo sapiens chromosome 1 clone RP11-66M4, 22 unordered pieces.
DEFINITION
ACCESSION AL360079
VERSION AL360079.3 GI:9801103
KEYWORDS HTG; HTGS PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS McIay,K.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Aug 14, 2000 this sequence version replaced gi:8919533.

COMMENT

----- Genome Center
Center: Sanger Centre
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bA66M4
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 1% of reads Chemistry:
Dye-terminator Big Dye; 98% of reads
Consensus quality: 145607 bases at least Q40
Consensus quality: 150854 bases at least Q30
Consensus quality: 153362 bases at least Q20
Insert size: 155370; sum-of-contigs
Insert size: 175368; 2.3% error; agarose-fp
Quality coverage: 3.40x in Q20 bases; sum-of-contigs Quality
coverage: 3.16x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 15108: contig of 15108 bp in length
* 15109 15208: gap of 100 bp
* 15209 20077: contig of 4869 bp in length
* 20078 20177: gap of 100 bp
* 20178 26598: contig of 6421 bp in length
* 26599 26698: gap of 100 bp
* 26699 31874: contig of 5176 bp in length
* 31875 31974: gap of 100 bp
* 31975 39580: contig of 7606 bp in length
* 39581 39680: gap of 100 bp
* 39681 62977: contig of 23297 bp in length
* 62978 63077: gap of 100 bp
* 63078 75654: contig of 12577 bp in length
* 75655 75754: gap of 100 bp
* 75755 90667: contig of 14913 bp in length
* 90668 90767: gap of 100 bp
* 90768 93945: contig of 3178 bp in length
* 93946 94045: gap of 100 bp
* 94046 99022: contig of 4977 bp in length
* 99023 99122: gap of 100 bp
* 99123 101699: contig of 2577 bp in length
* 101700 101799: gap of 100 bp
* 101800 105241: contig of 3442 bp in length
* 105242 105341: gap of 100 bp
* 105342 107538: contig of 2197 bp in length
* 107539 107638: gap of 100 bp
* 107639 110763: contig of 3370 bp in length
* 110764 111008: gap of 100 bp
* 111009 113755: contig of 2647 bp in length
* 113756 113855: gap of 100 bp
* 113856 121296: contig of 7441 bp in length
* 121297 121396: gap of 100 bp
* 121397 125841: contig of 4445 bp in length
* 125842 125941: gap of 100 bp
* 125942 129256: contig of 3315 bp in length
* 129257 129357: gap of 100 bp
* 129358 136269: contig of 6913 bp in length
* 136270 136369: gap of 100 bp
* 136370 138679: contig of 2510 bp in length
* 138680 138979: gap of 100 bp
* 138980 144504: contig of 5525 bp in length
* 144505 144604: gap of 100 bp

* 144605 157470: contig of 12866 bp in length.
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Matches 168; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CGGCAAACTCCCTGAATGTTTGGCAGTACTGACAGTACAGTTTCCCAATC 62
Db 15386 CTGCAAACTCCCTGAATGTTTGGCAGTACTGACAGTACAGTTTCCCAATC 15327
QY 63 CTCAACTCTGCTCCAGCTGATGAGGGGAGGAAAGGGATTACCTAGGGGTATGGCG 122
Db 15326 CTCACCTCTGCTCCAGCTGATGAGGGGAGGAAAGGGATTACCTAGGGGTATGGCG 15267
QY 123 ACCAATCTGAGTCCCACTGACAGCCGCGCCATCCCGAGCCTTGTGCTCAC 175
Db 15266 ACCATTCTGAGTCCCACTGACAGCCGCGCCATCCCGAGCCTTGTGCTCAC 15214

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Best Local Similarity 89.9%; Pred. No. 1.5e-32;
Matches 160; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

QY 1 CGCGGCAAAACTGCCGAAATGTGTTTGGCATCAGCTACTGACACGTAA-GGTTTCCCA 59
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QY 60 ATCCTCAACTCTCTGCTCTG--CCAGCTGATGAGGGGAAGAAAGGGAATTAACCTAGGGGTAT 117
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QY 118 GGGCGACCAATCTCTGAGTCCACCACTGACACGCCCATCCACGCTTTGTGCTCTAC 175
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RESULT 12
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LOCUS AX348874 5356 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 332 from Patent WO0202807.
ACCESSION AX348874
VERSION AX348874.1 GI:18614909
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of diseases associated with cell signalling
JOURNAL Patent: WO 0202807-A 332 10-JAN-2002;
Epigenomics AG (DE)

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source Location/Qualifiers
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/mol_type="unassigned DNA"
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/note="chemically treated genomic DNA (Homo sapiens) "

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Best Local Similarity 78.3%; Pred. No. 1.3e-26;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 CAAAACCTGCCGTAATCTGTTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCTC 65
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QY 66 AACTCTGTCCTGCAGCTGATGAGGGGAAGAAAGGGAATTAACCTAGGGGTATGGGCGACC 125
Db 1264 AACTCTATCTCTACCAACTAATAAAAAAAAAAAAAAAAAATTAACCTAAAAATATAAACGACC 1205

QY 126 AATCCTGAGTCCACCACTGACACGCCCATCCCGCTTTGTGCTCTAC 175
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RESULT 13
AX344469/c
LOCUS AX344469 5728 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 316 from Patent WO0200926.
ACCESSION AX344469
VERSION AX344469.1 GI:18492357
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of diseases associated with signal transduction
JOURNAL Patent: WO 0200926-A 316 03-JAN-2002;
Epigenomics AG (DE)

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Location/Qualifiers

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/mol_type="unassigned DNA"
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/note="chemically treated genomic DNA (Homo sapiens)"

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Best Local Similarity 78.2%; Pred. No. 1.3e-26;
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Db 969 CAAAACCTACCTAAATATATATTTTAACTACACTAAACGTAAATTTCCCAATCCTC 910

QY 66 AACTCTGTCCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGACC 125
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Db 909 AACTCTATCTTACCAACTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 850

QY 126 AATCTGAGTCCACCACTGACCGCCATCCCTCCAGCCTTGTGCTCAC 175
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Db 849 AATCTTAATCAACCACTAAACACCGCCATCCCTCCAGCCTTATACCTCAC 800

RESULT 14
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DEFINITION          Sequence 440 from Patent WO0168912.
ACCESSION            AX251472
VERSION              AX251472.1 GI:15984895
KEYWORDS
SOURCE               synthetic construct
ORGANISM              synthetic construct
                     artificial sequences.
REFERENCE
1
AUTHORS              Olek,A., Piepenbrock,C. and Berlin,K.
TITLE                Diagnosis of diseases associated with tumor suppressor genes and
                     oncogenes
JOURNAL              Patent: WO 0168912-A 440 20-SEP-2001;
                     Epigenomics AG (DE)
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/note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN
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Best Local Similarity 78.2%; Pred. No. 1.3e-26;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 CAAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAAGTTTCCCAATCCTC 65
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QY 66 AACTCTGTCCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGACC 125
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LOCUS                AX348873          5356 bp          DNA          linear          PAT 06-FEB-2002
DEFINITION          Sequence 331 from Patent WO0202807.
ACCESSION            AX348873
VERSION              AX348873.1 GI:18614908
KEYWORDS
SOURCE               synthetic construct

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ORGANISM              synthetic construct
                     artificial sequences.
REFERENCE
1
AUTHORS              Olek,A., Piepenbrock,C. and Berlin,K.
TITLE                Diagnosis of diseases associated with cell signalling
                     Patent: WO 0202807-A 331 10-JAN-2002;
                     Epigenomics AG (DE)
FEATURES
source
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/note="chemically treated genomic DNA (Homo sapiens)"

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Best Local Similarity 72.4%; Pred. No. 3.9e-21;
Matches 123; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 5 GCAAACTGCTGAAATGTTTGGCATCAGTACTGACACGTAAAGTTTCCCAATCCT 64
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QY 65 CAACTCTGCTCCTGCCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGCGAC 124
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QY 125 CAATCTGAGTCCACCACTGACCGCCATCCCGACGCTTGTGCTCA 174
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GenCore version 5.1.1.6
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Perfect score: 944
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Scoring table: IDENTITY_NUC
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Searched: 682709 seqs, 277475446 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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29 104.4 11.1 35408 3 US-09-563-869A-3 Sequence 3, Appli
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45 64.8 6.9 35081 2 US-08-752-760A-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-994-689C-3
; Sequence 3, Application US/08994689C
; Patent No. 6613958
; GENERAL INFORMATION:
; APPLICANT: Neuhold, Lisa
; APPLICANT: Killar, Loran
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
; TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,689C
; FILING DATE: 1997-12-19
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0630/0D532
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3479 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-994-689C-3

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Best Local Similarity 80.8%; Pred. No. 7.5e-35;
Matches 210; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY 410 CCGTGCCCGCCGCGCCGACCTTCATCGATTGGATTGGCGCGATGCTCCAGA 469

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RESULT 2
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; Sequence 9, Application US/08994689C
; Patent No. 6613958
; GENERAL INFORMATION:
; APPLICANT: Neuhold, Lisa
; APPLICANT: Killar, Loran
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
; TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,689C
; FILING DATE: 1997-12-19
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0630/0D532
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5276 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-994-689C-9

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Best Local Similarity 80.8%; Pred. No. 8.5e-35;
Matches 210; Conservative 0; Mismatches 49; Indels 1; Gaps 1;
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; Sequence 10, Application US/08994689C
; Patent No. 6613958
; GENERAL INFORMATION:
; APPLICANT: Neuhold, Lisa
; APPLICANT: Killar, Loran
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
; TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,689C
; FILING DATE: 1997-12-19
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0630/0D532
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7664 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-994-689C-10

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Best Local Similarity 80.8%; Pred. No. 9.5e-35;
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Db 1048 TGGCTGAAACCTGCGCTGTTATTTAACTGTTCTCTGAGAGCTGTGAATCGG 1107
QY 530 GCTCTGTATGCGTTGAGAAAGCCCATTCATGAGAGGCAAGCCAGTGGGT-CCCCC 588
Db 1108 GCTCTGTATGCGCTCGAGAAAGCCCATTCATGAGAGGCAAGCCAGTGGGTCCCCC 1167
QY 589 AACTCCCGGACCCCTCTCCCAATGACAGGCTCCCGCCCTCATCCCGCCCGCCAC 648
Db 1168 GACTCCCGGACCCCTCTCCCAATATATATCCCGCCCTGTCGCGCGCTGCGCCAC 1227
QY 649 CCCCCGCTGCGCGCTGCGC 668
Db 1228 CTCGCGGCTCGGCGCCGC 1247
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US-09-383-630-4
; Sequence 4, Application US/09383630A
; Patent No. 6265632
; GENERAL INFORMATION:
; APPLICANT: Avner Yayon et al.
; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
; FACTOR RECEPTOR ASSOCIATED
; CHONDRODYSPLASIA
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted
; to an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,630A
; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 1402/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8083
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Query Match 15.3%; Score 144; DB 3; Length 8083;
Best Local Similarity 96.7%; Pred. No. 4.6e-28;
Matches 147; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 732 TAGTGGATCCCCGGCTGCAGATCTGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGAT 791
Db 4867 TAGTGGATCCCCGGCTGCAGATCCCCCGGCGCAGTAGTCCAGGGTTTCCTTGATGAT 4926
QY 792 GTCATACTTATCTGTCCTCTTTTTCACAGCTCGCGTTGAGGACAAACTCTTCGCG 851

Db 4927 GTCATACTTATCTGTCCTCTTTTTCACAGCTCGCGTTGAGGACAAACTCTTCGCG 4986
QY 852 GTCTTTCCAGTGGGATCGACGGTATCGATAA 883
Db 4987 GTCTTTCCAGTGGGATCGACGGTATCGATCA 5018
RESULT 5
US-09-383-630-5
; Sequence 5, Application US/09383630A
; Patent No. 6265632
; GENERAL INFORMATION:
; APPLICANT: Avner Yayon et al.
; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
; FACTOR RECEPTOR ASSOCIATED
; CHONDRODYSPLASIA
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted
; to an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,630A
; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 1402/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8083
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-383-630-5
Query Match 15.3%; Score 144; DB 3; Length 8083;
Best Local Similarity 96.7%; Pred. No. 4.6e-28;
Matches 147; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 732 TAGTGGATCCCCGGCTGCAGATCTGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGAT 791
Db 4867 TAGTGGATCCCCGGCTGCAGATCCCCCGGCGCAGTAGTCCAGGGTTTCCTTGATGAT 4926
QY 792 GTCATACTTATCTGTCCTCTTTTTCACAGCTCGCGTTGAGGACAAACTCTTCGCG 851
Db 4927 GTCATACTTATCTGTCCTCTTTTTCACAGCTCGCGTTGAGGACAAACTCTTCGCG 4986
QY 852 GTCTTTCCAGTGGGATCGACGGTATCGATAA 883
Db 4987 GTCTTTCCAGTGGGATCGACGGTATCGATCA 5018

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RESULT 6
US-09-857-063-16
; Sequence 16, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-16

Query Match      12.1%; Score 114.2; DB 4; Length 246;
Best Local Similarity 87.4%; Pred. No. 9.4e-21;
Matches 125; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 727 AGCTCTAGTGATGCCCGGGCTGCAGATCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 786
Db 103 AGCACTTCTGCAGCCCAAGCTTGTCAGCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 162
QY 787 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 846
Db 163 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 222
QY 847 TCGCGGTCTTCCAGTGGGATC 869
Db 223 TCGCGGTCTTCCAGTGGGATC 245

RESULT 7
US-09-857-063-5
; Sequence 5, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-5

Query Match      12.1%; Score 114.2; DB 4; Length 246;
Best Local Similarity 87.4%; Pred. No. 9.4e-21;
Matches 125; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 727 AGCTCTAGTGATGCCCGGGCTGCAGATCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 786
Db 103 AGCACTTCTGCAGCCCAAGCTTGTCAGCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 162
QY 787 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 846
Db 163 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 222
QY 847 TCGCGGTCTTCCAGTGGGATC 869
Db 223 TCGCGGTCTTCCAGTGGGATC 245

RESULT 8
US-09-857-063-14
; Sequence 14, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-14

Query Match      12.0%; Score 113; DB 4; Length 244;
Best Local Similarity 95.9%; Pred. No. 1.9e-20;
Matches 116; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 757 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATCTATCTCTGTCCTTTT 816
Db 85 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATCTATCTCTGTCCTTTT 144
QY 817 TTCCACAGCTCGGGTTGAGGACAACTCTTCGCGGTCTTCCAGTGGGATCGACGTA 876
Db 145 TTCCACAGCTCGGGTTGAGGACAACTCTTCGCGGTCTTCCAGTGGGATCGACGTA 204
QY 877 T 877
Db 205 T 205

RESULT 9
US-09-857-063-3
; Sequence 3, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-3

Query Match      12.0%; Score 113; DB 4; Length 244;
Best Local Similarity 95.9%; Pred. No. 1.9e-20;
Matches 116; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 757 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATCTATCTCTGTCCTTTT 816
Db 85 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATCTATCTCTGTCCTTTT 144
QY 817 TTCCACAGCTCGGGTTGAGGACAACTCTTCGCGGTCTTCCAGTGGGATCGACGTA 876
Db 145 TTCCACAGCTCGGGTTGAGGACAACTCTTCGCGGTCTTCCAGTGGGATCGACGTA 204
QY 877 T 877
Db 205 T 205
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US-09-857-063-5
Query Match      12.1%; Score 114.2; DB 4; Length 282;
Best Local Similarity 87.4%; Pred. No. 9.7e-21;
Matches 125; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 727 AGCTCTAGTGATGCCCGGGCTGCAGATCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 786
Db 139 AGCACTTCTGCAGCCCAAGCTTGTCAGCTGTAGGGCGCAGTAGTCCAGGGTTTCCTTG 198
QY 787 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 846
Db 139 ATGATGTCACTATCTCTGTCCTTTTTCACAGCTCGGGTTGAGGACAACTCT 258
QY 847 TCGCGGTCTTCCAGTGGGATC 869
Db 259 TCGCGGTCTTCCAGTGGGATC 281

RESULT 8
US-09-857-063-14
; Sequence 14, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
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; SEQ ID NO 14
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-14

Query Match      12.0%; Score 113; DB 4; Length 244;
Best Local Similarity 95.9%; Pred. No. 1.9e-20;
Matches 116; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 757 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATCTATCTCTGTCCTTTT 816
Db 85 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATCTATCTCTGTCCTTTT 144
QY 817 TTCCACAGCTCGGGTTGAGGACAACTCTTCGCGGTCTTCCAGTGGGATCGACGTA 876
Db 145 TTCCACAGCTCGGGTTGAGGACAACTCTTCGCGGTCTTCCAGTGGGATCGACGTA 204
QY 877 T 877
Db 205 T 205

RESULT 9
US-09-857-063-3
; Sequence 3, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
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; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-3

Query Match      12.0%; Score 113; DB 4; Length 244;
Best Local Similarity 95.9%; Pred. No. 1.9e-20;
Matches 116; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-24

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QY 817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTGGGGATCGACGGT 875
DB 148 TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGGTCTTTCCAGTGGGGATCGGGAT 206

RESULT 13
US-09-857-063-12
; Sequence 12, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-12

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Matches 115; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTGGGGATCGACGGT 875
DB 184 TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGGTCTTTCCAGTGGGGATCGGGAT 242

RESULT 14
US-09-857-063-17
; Sequence 17, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
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; CURRENT APPLICATION NUMBER: US/09/857,063
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 247
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-17

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Best Local Similarity 99.1%; Pred. No. 5e-20;
Matches 112; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTGGGGATC 869
DB 194 TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGGTCTTTCCAGTGGGGATC 246

RESULT 15
US-09-857-063-18
; Sequence 18, Application US/09857063
; Patent No. 6579681
; GENERAL INFORMATION:
; APPLICANT: Huls, Christoph
; APPLICANT: Bauer, Bettina
; APPLICANT: Simandi, Claus
; APPLICANT: Luhrmann, Reinhard
; APPLICANT: Achsel, Tilmann
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: Test System for Detecting a Splicing Reaction and Use Thereof
; FILE REFERENCE: 199at.01.us (8602*34)
; CURRENT APPLICATION NUMBER: US/09/857,063
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PCT/EP00/01595
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: DE 199 09 156.0
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pre-mRNA
US-09-857-063-18

Query Match      11.8%; Score 111.4; DB 4; Length 256;
Best Local Similarity 99.1%; Pred. No. 5.1e-20;
Matches 112; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 757 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGCATATCTATCTGTCCTCTTTT 816
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QY 817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTGGGGATC 869
DB 203 TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGGTCTTTCCAGTGGGGATC 255

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Mon Sep 13 07:48:11 2004

us-09-808-388-7.sept04.rni

Page 7

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OM nucleic - nucleic search, using sw model

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(without alignments)
5187.326 Million cell updates/sec

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Perfect score: 944
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Post-processing: Minimum Match 0%

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- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	169.6	18.0	5276	15	US-10-375-884-9
4	169.6	18.0	7664	15	US-10-375-884-10
5	122.4	13.0	5887	15	US-10-277-161-73
6	104.4	11.1	1240	9	US-09-847-101B-28
7	104.4	11.1	1240	10	US-09-482-682-32
8	104.4	11.1	7231	9	US-09-847-101B-42
9	104.4	11.1	7231	10	US-09-482-682-64
10	104.4	11.1	7960	9	US-09-847-101B-30
11	104.4	11.1	7960	10	US-09-482-682-44
12	104.4	11.1	7989	9	US-09-847-101B-33
13	104.4	11.1	7989	10	US-09-482-682-47
14	104.4	11.1	8383	9	US-09-847-101B-29

15	104.4	11.1	8383	10	US-09-482-682-43	Sequence 43, Appl
16	104.4	11.1	8484	10	US-09-482-682-65	Sequence 65, Appl
17	104.4	11.1	10491	15	US-10-359-050-18	Sequence 18, Appl
18	104.4	11.1	11784	15	US-10-359-050-20	Sequence 20, Appl
19	104.4	11.1	11784	16	US-10-014-099F-106	Sequence 106, App
20	104.4	11.1	12538	15	US-10-359-050-13	Sequence 13, Appl
21	104.4	11.1	12645	15	US-10-359-050-13	Sequence 4, Appl
22	104.4	11.1	30365	13	US-10-384-136-4	Sequence 12, Appl
23	104.4	11.1	31183	17	US-10-431-598-19	Sequence 4, Appl
24	104.4	11.1	31672	13	US-10-384-136-3	Sequence 19, Appl
25	104.4	11.1	31880	16	US-10-427-717-507	Sequence 3, Appl
26	104.4	11.1	32480	9	US-09-847-101B-23	Sequence 507, App
27	104.4	11.1	32480	10	US-09-482-682-27	Sequence 23, Appl
28	104.4	11.1	32798	15	US-10-424-638-1	Sequence 27, Appl
29	104.4	11.1	33622	16	US-10-403-337-44	Sequence 1, Appl
30	104.4	11.1	33622	16	US-10-351-890-44	Sequence 44, Appl
31	104.4	11.1	33855	16	US-10-383-846-5	Sequence 5, Appl
32	104.4	11.1	34427	10	US-09-111-911-5	Sequence 479, App
33	104.4	11.1	34555	15	US-10-117-982-479	Sequence 1, Appl
34	104.4	11.1	34555	16	US-10-313-986-479	Sequence 43, Appl
35	104.4	11.1	34573	16	US-10-383-846-1	Sequence 3, Appl
36	104.4	11.1	34616	13	US-10-384-136-2	Sequence 2, Appl
37	104.4	11.1	35211	16	US-10-403-337-43	Sequence 43, Appl
38	104.4	11.1	35211	16	US-10-351-890-43	Sequence 3, Appl
39	104.4	11.1	35408	15	US-10-155-649-3	Sequence 2, Appl
40	104.4	11.1	35871	9	US-09-956-335-2	Sequence 43, Appl
41	104.4	11.1	35935	9	US-09-725-720-43	Sequence 4, Appl
42	104.4	11.1	35935	9	US-09-782-378A-4	Sequence 5, Appl
43	104.4	11.1	35935	9	US-09-782-378A-5	Sequence 12, Appl
44	104.4	11.1	35935	10	US-09-739-007-43	
45	104.4	11.1	35935	17	US-10-264-839-12	

ALIGNMENTS

RESULT 1

US-09-808-388-7
; Sequence 7, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 944
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence conferring specificity of expression
US-09-808-388-7

Query Match 100.0%; Score 944; DB 9; Length 944;
Best Local Similarity 100.0%; Pred. No. 4.4e-272;
Matches 944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTGGCCCTCGGGTACGCCCTGATCCGCTCGGGCTCCCGAGTCGCTGCTGCTGA 60
DB 1 TCCTGGCCCTCGGGTACGCCCTGATCCGCTCGGGCTCCCGAGTCGCTGCTGCTGA 60

QY	61	CGCTGCTCATCGCCGCGTCTCTACGGTCTAGGCGCAGGATGCGCGTAAAGTCGCCGCGC	120
Db	61	CGCTGCTCATCGCCGCGTCTCTACGGTCTAGGCGCAGGATGCGCGTAAAGTCGCCGCGC	120
QY	121	CCCTGCTACTCTCCCTGACTGTGACCCCTTTCTCTCTACTCTCCCTCCCAAGTACTAG	180
Db	121	CCCTGCTACTCTCCCTGACTGTGACCCCTTTCTCTCTACTCTCCCTCCCAAGTACTAG	180
QY	181	GATCCCCCTAGAGCTTGAGATCTGGGATTTGGCAGCATGGCTTCCAGATGGCTGAAAC	240
Db	181	GATCCCCCTAGAGCTTGAGATCTGGGATTTGGCAGCATGGCTTCCAGATGGCTGAAAC	240
QY	241	CCTGCCCTATTTATTTAAACTGTTCTCTGTTGAGAGCTGTGAATCGGCTCTGTATGC	300
Db	241	CCTGCCCTATTTATTTAAACTGTTCTCTGTTGAGAGCTGTGAATCGGCTCTGTATGC	300
QY	301	GCTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTCTCCCAACTCCCGGACC	360
Db	301	GCTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTCTCCCAACTCCCGGACC	360
QY	361	CCCTCTCCCAATGACAGCTCCCGCCCTCATCCCTCCCAAGGCCAGTGGTCTCCCAACTCCCGGACC	420
Db	361	CCCTCTCCCAATGACAGCTCCCGCCCTCATCCCTCCCAAGGCCAGTGGTCTCCCAACTCCCGGACC	420
QY	421	CTGCCGCCACCTTCAGATCGATCTGGGATTTGGCAGCATGGCTTCCAGATGGCTGAAAC	480
Db	421	CTGCCGCCACCTTCAGATCGATCTGGGATTTGGCAGCATGGCTTCCAGATGGCTGAAAC	480
QY	481	CTGCCGCCATTTATTTAACTGTTCTCTGTTGAGAGCTGTGAATCGGCTCTGTATGC	540
Db	481	CTGCCGCCATTTATTTAACTGTTCTCTGTTGAGAGCTGTGAATCGGCTCTGTATGC	540
QY	541	GCTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTCTCCCAACTCCCGGACC	600
Db	541	GCTTGAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGTCTCCCAACTCCCGGACC	600
QY	601	CCCTCTCCCAATGACAGCTCCCGCCCTCATCCCTCCCAAGGCCAGTGGTCTCCCAACTCCCGGACC	660
Db	601	CCCTCTCCCAATGACAGCTCCCGCCCTCATCCCTCCCAAGGCCAGTGGTCTCCCAACTCCCGGACC	660
QY	661	CTGCCGCCACCTTCAGATCGATCTGGGATTTGGCAGCATGGCTTCCAGATGGCTGAAAC	720
Db	661	CTGCCGCCACCTTCAGATCGATCTGGGATTTGGCAGCATGGCTTCCAGATGGCTGAAAC	720
QY	721	AAGCCAAAGCTCTAGTGTATCCCCGGGCTGCAGATCTGTAGGGCGAGTAGTCCAGGTT	780
Db	721	AAGCCAAAGCTCTAGTGTATCCCCGGGCTGCAGATCTGTAGGGCGAGTAGTCCAGGTT	780
QY	781	TCCTTGATGATGTCATCTTATCTGTCCTTTTTCACAGCTCGCGGTTGAGGACA	840
Db	781	TCCTTGATGATGTCATCTTATCTGTCCTTTTTCACAGCTCGCGGTTGAGGACA	840
QY	841	AACCTTTCGGGTTCTTCCAGTGGGATCGACGATCGATTAAGCTTGATGATCTGTGAC	900
Db	841	AACCTTTCGGGTTCTTCCAGTGGGATCGACGATCGATTAAGCTTGATGATCTGTGAC	900
QY	901	ATGCGGATCCCGTCTGTTTACAACTGTCGACGTGGGAAACCC	944
Db	901	ATGCGGATCCCGTCTGTTTACAACTGTCGACGTGGGAAACCC	944
RESULT 2			
US-10-375-884-3			
; Sequence 3, Application US/10375884			
; Publication No. US20030159165A1			
; GENERAL INFORMATION:			
; APPLICANT: NEUHOLD, Lisa A.			
; APPLICANT: KILLAR, Loran Marie			
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR DEGENERATIVE DISEASES OF CARTILAGE			
; FILE REFERENCE: 0630/1D532US2			
; CURRENT APPLICATION NUMBER: US/10/375,884			
; CURRENT FILING DATE: 2003-02-27			
; PRIOR APPLICATION NUMBER: US 08/994,689			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 9			
; LENGTH: 5276			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: transgene			
US-10-375-884-9			
Query Match 18.0%; Score 169.6; DB 15; Length 5276;			
Best Local Similarity 80.8%; Pred. No. 3.7e-40;			
Matches 210; Conservative 0; Mismatches 49; Indels 1; Gaps 1;			
QY	410	CCCGTCCCGCTGCGCCACCTTCAGATCGATCTGGGATTTGGCAGCATGGCTTCCAGA	469
Db	988	CTCAGTCTCTCTTTGTAGAGCTTGTTCGTTGAGGATTTGGCAGCATGGCTTCCAGA	1047
QY	470	TGGCTGAAACCCCTGCGCGTATTTATTAACCTGGTCTCTGTTGAGAGCTGTGAATCGG	529
Db	1048	TGGCTGAAACCCCTGCGCGTATTTATTAACCTGGTCTCTGTTGAGAGCTGTGAATCGG	1107
QY	530	GCTCTGTATGGCTTGAAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGCTTCCGCCAC	588
Db	530	GCTCTGTATGGCTTGAAGAAAGCCCATTCATGAGAGCAAGGCCAGTGGCTTCCGCCAC	588

US-10-277-161-73
Sequence 73, Application US/10277161
Publication No. US20030194696A1
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
APPLICANT: Smith, Ernest S.
TITLE OF INVENTION: Methods of Producing a Library and Methods of Selecting Polynucle
TITLE OF INVENTION: of Interest
FILE REFERENCE: 1821.0050006
CURRENT APPLICATION NUMBER: US/10/277,161
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 60/192,586
PRIOR FILING DATE: 2000-03-28

```
US-09-482-682-32
; Sequence 32, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: adenovirus
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-32

Query Match 11.1%; Score 104.4; DB 10; Length 1240;
Best Local Similarity 99.1%; Pred. No. 8.3e-21; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 1;

QY 757 TGTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTATCTGTCCTCTTTT 816
Db 1001 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTATCTGTCCTCTTTT 1060

QY 817 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 862
Db 1061 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 1106

RESULT 8
US-09-847-101B-42
; Sequence 42, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 42
; LENGTH: 7231
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pdv80
US-09-847-101B-42

Query Match 11.1%; Score 104.4; DB 9; Length 7231;
Best Local Similarity 99.1%; Pred. No. 1.3e-20; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 1;

QY 757 TGTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 816
Db 1849 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 1908

QY 817 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 862
Db 1909 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 1954

RESULT 9
US-09-847-101B-42
; Sequence 42, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 42
; LENGTH: 7231
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pdv80
US-09-847-101B-42

Query Match 11.1%; Score 104.4; DB 9; Length 7231;
Best Local Similarity 99.1%; Pred. No. 1.3e-20; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 1;

QY 757 TGTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 816
Db 1849 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 1908

QY 817 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 862
Db 1909 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 1954
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US-09-482-682-64
; Sequence 64, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 64
; LENGTH: 7231
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-64

Query Match 11.1%; Score 104.4; DB 10; Length 7231;
Best Local Similarity 99.1%; Pred. No. 1.3e-20; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 1;

QY 757 TGTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 816
Db 1849 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 1908

QY 817 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 862
Db 1909 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 1954

RESULT 10
US-09-847-101B-30
; Sequence 30, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 7960
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pdv67
US-09-847-101B-30

Query Match 11.1%; Score 104.4; DB 9; Length 7960;
Best Local Similarity 99.1%; Pred. No. 1.3e-20; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 1;

QY 757 TGTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 816
Db 1929 TCTAGGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTGTCCTCTTTT 1988

QY 817 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 862
Db 1989 TTCCACAGCTCGCGTTGAGGACAACTCTTCGCGGTCTTTCCAGT 2034
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RESULT 11
US-09-482-682-44
; Sequence 44, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 44
; LENGTH: 7960
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-44

Query Match          11.1%; Score 104.4; DB 10; Length 7960;
Best Local Similarity 99.1%; Pred. No. 1.3e-20;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      757 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTCTGTCCTCTTTT 816
Db      1929 TCTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTCTGTCCTCTTTT 1988

QY      817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 862
Db      1989 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 2034

RESULT 12
US-09-847-101B-33
; Sequence 33, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4242
; OTHER INFORMATION: N is any
; NAME/KEY: misc_feature
; LOCATION: 4245
; OTHER INFORMATION: N is any
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pDV69
US-09-847-101B-33

Query Match          11.1%; Score 104.4; DB 9; Length 7989;
Best Local Similarity 99.1%; Pred. No. 1.3e-20;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      757 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTCTGTCCTCTTTT 816
Db      1929 TCTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTCTGTCCTCTTTT 1988

QY      817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 862
Db      1989 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 2034

RESULT 13
US-09-482-682-47
; Sequence 47, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-47

Query Match          11.1%; Score 104.4; DB 10; Length 7989;
Best Local Similarity 99.1%; Pred. No. 1.3e-20;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      757 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTCTGTCCTCTTTT 816
Db      1929 TCTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTCTGTCCTCTTTT 1988

QY      817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 862
Db      1989 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 2034

RESULT 14
US-09-847-101B-29
; Sequence 29, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 8383
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pDV60
US-09-847-101B-29

Query Match          11.1%; Score 104.4; DB 9; Length 8383;
Best Local Similarity 99.1%; Pred. No. 1.4e-20;

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QY      757 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTCTGTCCTCTTTT 816
Db      1929 TCTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTCTGTCCTCTTTT 1988

QY      817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 862
Db      1989 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 2034

RESULT 13
US-09-482-682-47
; Sequence 47, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-47

Query Match          11.1%; Score 104.4; DB 10; Length 7989;
Best Local Similarity 99.1%; Pred. No. 1.3e-20;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      757 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTCTGTCCTCTTTT 816
Db      1929 TCTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATATCTCTGTCCTCTTTT 1988

QY      817 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 862
Db      1989 TTCCACAGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT 2034

RESULT 14
US-09-847-101B-29
; Sequence 29, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 8383
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pDV60
US-09-847-101B-29

Query Match          11.1%; Score 104.4; DB 9; Length 8383;
Best Local Similarity 99.1%; Pred. No. 1.4e-20;

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Mon Sep 13 07:48:12 2004

Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 757 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATACCTATCCTGTCCTCTTTT 816

Db 1907 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATACCTATCCTGTCCTCTTTT 1966

QY 817 TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGTCTTTCCAGT 862

Db 1967 TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGTCTTTCCAGT 2012

RESULT 15

US-09-482-682-43

; Sequence 43, Application US/09482682

; Publication No. US20030157688A1

; GENERAL INFORMATION:

; APPLICANT: VON SEGGERN, DANIEL

; APPLICANT: NEMEROW, GLEN R.

; APPLICANT: HALLENBECK, PAUL

; APPLICANT: STEVENSON, SUSAN

; APPLICANT: SKRIPCHENKO, YELENA

; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,

; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE

; FILE REFERENCE: 1294.0010001

; CURRENT APPLICATION NUMBER: US/09/482,682

; CURRENT FILING DATE: 2000-01-14

; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 43

; LENGTH: 8383

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: plasmid

US-09-482-682-43

Query Match 11.1%; Score 104.4; DB 10; Length 8383;

Best Local Similarity 99.1%; Pred. No. 1.4e-20;

Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 757 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATACCTATCCTGTCCTCTTTT 816

Db 1907 TGTAGGCGCAGTAGTCCAGGGTTTCCTTGATGATGTCATACCTATCCTGTCCTCTTTT 1966

QY 817 TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGTCTTTCCAGT 862

Db 1967 TTCCACAGCTCGCGGTTGAGGACAACTCTTCGCGTCTTTCCAGT 2012

Search completed: September 11, 2004, 14:11:20

Job time : 917.647 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 09:20:47 ; Search time 322.028 Seconds
(without alignments)
5187.326 Million cell updates/sec

Title: US-09-808-388-6

Perfect score: 332

Sequence: 1 gtaccaattgcacaaacta.....caactctggagctctctgag 332

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10C_NEW PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	100.0	332	9	US-09-808-388-6
2	271	81.6	271	9	US-09-808-388-5
3	213	64.2	1080	10	US-09-865-866-17
4	165	49.7	6083	13	US-10-221-714A-440
5	150.2	45.2	6083	13	US-10-221-714A-439
6	118.8	35.8	967	15	US-10-210-120-75
7	84.4	25.4	3330	9	US-09-917-800A-1495
8	84.4	25.4	3330	12	US-10-152-319A-2157
9	84.4	25.4	3330	16	US-10-191-803-398
10	80.8	24.3	1076	9	US-09-925-300-70
11	50	15.1	735	9	US-09-981-353-17
12	49.6	14.9	4990	10	US-09-865-866-97
13	41	12.3	41	9	US-09-808-388-3
14	34.2	10.3	371	15	US-10-387-495-8
15					Sequence 6, Appli
					Sequence 5, Appli
					Sequence 17, Appl
					Sequence 440, App
					Sequence 439, App
					Sequence 75, Appl
					Sequence 1495, Ap
					Sequence 2157, Ap
					Sequence 398, App
					Sequence 70, Appl
					Sequence 97, Appl
					Sequence 3, Appli
					Sequence 8, Appli

c	15	34.2	10.3	742	13	US-10-027-632-151276	Sequence 151276,
c	16	34.2	10.3	742	16	US-10-027-632-151276	Sequence 151276,
	17	33.8	10.2	420	15	US-10-422-264-17	Sequence 17, Appl
	18	33.8	10.2	1441	15	US-10-422-264-13	Sequence 13, Appl
	19	33.8	10.2	2136	9	US-09-862-658-3	Sequence 3, Appli
	20	33.8	10.2	2136	15	US-10-175-696-24	Sequence 24, Appl
	21	33.8	10.2	2136	17	US-10-776-871-24	Sequence 24, Appl
	22	33.8	10.2	2236	15	US-10-422-264-5	Sequence 5, Appli
	23	33.8	10.2	2307	13	US-10-302-172-803	Sequence 803, App
	24	33.8	10.2	2604	15	US-10-422-264-23	Sequence 23, Appli
	25	33.8	10.2	2701	15	US-10-422-264-1	Sequence 1, Appli
	26	33.8	10.2	3320	9	US-09-862-658-1	Sequence 1, Appli
	27	33.8	10.2	3320	15	US-10-175-696-22	Sequence 22, Appl
	28	33.8	10.2	3320	17	US-10-776-871-22	Sequence 22, Appl
	29	33.8	10.2	3384	15	US-10-422-264-29	Sequence 29, Appl
	30	33.2	10.0	2835	16	US-10-104-047-1501	Sequence 1501, Ap
c	31	33	9.9	343	17	US-10-767-701-23550	Sequence 23550, A
	32	32.6	9.8	54552	13	US-10-087-192-1303	Sequence 1303, Ap
	33	32.4	9.8	819	16	US-10-027-632-130312	Sequence 130312,
c	34	32.4	9.8	819	16	US-10-027-632-130312	Sequence 130312,
	35	32.4	9.8	94529	16	US-10-034-650-52	Sequence 52, Appl
	36	32.2	9.7	573	13	US-10-027-632-50048	Sequence 50048, A
	37	32.2	9.7	573	13	US-10-027-632-50049	Sequence 50049, A
	38	32.2	9.7	573	13	US-10-027-632-69880	Sequence 69880, A
	39	32.2	9.7	573	13	US-10-027-632-69881	Sequence 69881, A
	40	32.2	9.7	573	13	US-10-027-632-70565	Sequence 70565, A
	41	32.2	9.7	573	13	US-10-027-632-70566	Sequence 70566, A
	42	32.2	9.7	573	16	US-10-027-632-50048	Sequence 50048, A
	43	32.2	9.7	573	16	US-10-027-632-50049	Sequence 50049, A
	44	32.2	9.7	573	16	US-10-027-632-69880	Sequence 69880, A
	45	32.2	9.7	573	16	US-10-027-632-69881	Sequence 69881, A

ALIGNMENTS

RESULT 1
US-09-808-388-6
Sequence 6, Application US/09808388
Patent No. US20020081719A1

GENERAL INFORMATION:
APPLICANT: Massaad, Charbel
APPLICANT: Berenbaum, Francis
APPLICANT: Olivier, Jean-Luc
APPLICANT: Salvat, Colette
APPLICANT: Berezziat, Gilbert
TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
TITLE OF INVENTION: their uses
FILE REFERENCE: SI00010
CURRENT APPLICATION NUMBER: US/09/808,388
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: FR/00/03262
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: US 60/196,959
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6

LENGTH: 332
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PPPE/PLA2s hybrid promoter
US-09-808-388-6

Query Match 100.0%; Score 332; DB 9; Length 332;
Best Local Similarity 100.0%; Pred.No. 1.8e-106;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query 1 GTACCAATTCGACAAACTAGTCAAGGTCAATCAAACTAGTCAAGGTCAAAATTCGA 60
Db 1 GTACCAATTCGACAAACTAGTCAAGGTCAATCAAACTAGTCAAGGTCAAAATTCGA 60

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QY 61 ACGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACAGTAAGGTTCCCA 120
Db 61 ACGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACAGTAAGGTTCCCA 120
QY 121 ATCTCAACTCTGCTCCAGCTGATGAGGGGAGGAAGGATACCTAGGGGTATGG 180
Db 121 ATCTCAACTCTGCTCCAGCTGATGAGGGGAGGAAGGATACCTAGGGGTATGG 180
QY 181 GCGACCAATCTGAGTCCACCACTGACCGCCCATCCCCAGCTTGTGCTCACCTAC 240
Db 181 GCGACCAATCTGAGTCCACCACTGACCGCCCATCCCCAGCTTGTGCTCACCTAC 240
QY 241 CCCCACCTCCAGAGGAGCAGCTATTATTAGGGGAGCAGGATGCGAACAACAGAC 300
Db 241 CCCCACCTCCAGAGGAGCAGCTATTATTAGGGGAGCAGGATGCGAACAACAGAC 300
QY 301 GGCCTGGGGATACAACTCTGAGTCTCTGAG 332
Db 301 GGCCTGGGGATACAACTCTGAGTCTCTGAG 332

RESULT 2
US-09-808-388-5
; Sequence 5, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment of the PLA2s promoter
US-09-808-388-5
Query Match 81.6%; Score 271; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 5.6e-85;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 62 CCGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACAGTAAGGTTCCCA 121
Db 1 CCGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACAGTAAGGTTCCCA 60
QY 122 TCCTCAACTCTGCTCCAGCTGATGAGGGGAGGAAGGATACCTAGGGGTATGG 181
Db 61 TCCTCAACTCTGCTCCAGCTGATGAGGGGAGGAAGGATACCTAGGGGTATGG 120
QY 182 CGACCAATCTGAGTCCACCACTGACCGCCCATCCCCAGCTTGTGCTCACCTACC 241
Db 121 CGACCAATCTGAGTCCACCACTGACCGCCCATCCCCAGCTTGTGCTCACCTACC 180
QY 242 CCAACCTCCAGAGGAGCAGCTATTATTAGGGGAGCAGGATGCGAACAACAGAC 301
Db 181 CCAACCTCCAGAGGAGCAGCTATTATTAGGGGAGCAGGATGCGAACAACAGAC 240
QY 302 GGCCTGGGGATACAACTCTGAGTCTCTGAG 332
Db 241 GGCCTGGGGATACAACTCTGAGTCTCTGAG 271
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RESULT 3
US-09-865-866-17
; Sequence 17, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 17
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-865-866-17
Query Match 64.2%; Score 213; DB 10; Length 1080;
Best Local Similarity 93.1%; Pred. No. 3e-64;
Matches 256; Conservative 0; Mismatches 15; Indels 4; Gaps 3;
QY 61 ACGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACAGTAAGG-TTTCCT 119
Db 762 ACTCGGCAAACTGCCTGAAATGTGTTTGGCATCAGGCTACTGACACGTAAGGGTTTCCC 821
QY 120 AATCCTCAACTCTGCTCTG--CCAGCTGATGAGGGGAGGAAGGGATTACCTAGGGTA 177
Db 822 AATCCTCAACTCTGCTCTGGCAGGCTGATGAGGGGAGGAAGGGATTACCTAGGGTA 881
QY 178 TGGGGACCAATCCTGAGTCCACCACTGACACGCCCATCCCAGCTTGTGCTCACC 237
Db 882 TGGGGACCAATCCTGAGTCCACCACTGACACGCCCATCCCAGCTTGTGCTCACC 941
QY 238 TACCCCAACCTCCAGAGGAGCAGCTATTATTAGGGGAGCAGGATGCGAACAACAA 297
Db 942 TACCCCAACCT-CCAGAGGAGCAGCTATTATTAGGGGAGCAGGATGCGAACAACAA 1000
QY 298 GACGGCCTGGGATACAACTCTGGAGTCTCTGAG 332
Db 1001 GACGGCCTGGGATACAACTCTGGAGTCTCTGAG 1035

RESULT 4
US-10-221-714A-440/c
; Sequence 440, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013,1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 440
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; LENGTH: 6083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-440

Query Match          49.7%; Score 165; DB 13; Length 6083;
Best Local Similarity 74.7%; Pred. No. 5.7e-47;
Matches 207; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 55 ATTGGAAGCGGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAGGT 114
   |||||
Db 1336 ATAAAAAACTACAAAACCTACTAAATATATTTTAAATCACTACTAAGACGTAAT 1277

QY 115 TTCCCAATCCTCAACTGCTGCTGCGACGCTGATGAGGGAAGGATTAACCTAGG 174
   |||||
Db 1276 TTCCCAATCCTCAACTGCTGCTGCGACGCTGATGAGGGAAGGATTAACCTAGG 174

QY 175 GTATGGGCGACCAATCCTGAGTCCACCACTGACACGCCCATCCCGAGCCTTGTGCTC 234
   |||||
Db 1216 ATATAAGGACCAATCTTAATTCACCACTAATCCACGCCCATCCCGAGCCTTGTGCTC 1157

QY 235 ACCTACCCCACTCCAGAGGAGAGCTATTTAAGGGGAGGAGGAGTGCGAGACAAA 294
   |||||
Db 1156 ACCTACCCCACTCCAGAGGAGAGCTATTTAAGGGGAGGAGGAGTGCGAGACAAA 1097

QY 295 CAAGACGCCCTGGGATACAACTCTGGAGTCTCTGA 331
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Db 1096 CAAGACGCCCTGGGATACAACTCTGGAGTCTCTGA 1060

RESULT 5
US-10-221-714A-439
; Sequence 439, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BEELIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 439
; LENGTH: 6083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-439

Query Match          45.2%; Score 150.2; DB 13; Length 6083;
Best Local Similarity 72.7%; Pred. No. 9.5e-42;
Matches 194; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 66 GCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCT 125
   |||||
Db 4759 GTAAAAATGTTGAAATGTTTGGTATTAGTTATTGATACGTAAGGTTTATTATTTT 4818
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QY 126 CAACTCTCTCTGCGACGCTGATGAGGGAAGAAAGGATTAACCTAGGGTATGGCGAC 185
   |||||
Db 4819 TAAATTTGTTTGTAGTTGATGAGGGAAGAAAGGATTAATTTAGGGTATGGCGAT 4878

QY 186 CAATCTGAGTCCCACTGACACGCCCATCCAGCCTTGTGCTCACCCTACCCCA 245
   |||||
Db 4879 TAAATTTGAGTTTAAATTAATGATTACGTTTATTTTAGTTTGTGTTTATTTTATTTTA 4938

QY 246 ACCTCCCAAGAGGAGCAGCTATTTAAGGGAGGAGAGTGAGACAAACAGACGGCT 305
   |||||
Db 4939 ATTTTATAGAGGAGTAGTTATTTAAGGGAGTAGGAGTAGAATAAATAAGACGGTT 4998

QY 306 GGGGATACAACTCTGGAGTCTCTGAG 332
   |||||
Db 4999 GGGGATATAATTTTGGAGTTTTTTGAG 5025

RESULT 6
US-10-210-120-75
; Sequence 75, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-75

Query Match          35.8%; Score 118.8; DB 15; Length 967;
Best Local Similarity 83.3%; Pred. No. 5.1e-31;
Matches 135; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 171 AGGGTATGGCGACCAATCCTGAGTCCACCACTGACAGGCCCATCCCGAGCCTTGTG 230
   |||||
Db 3 AGGAAAAGAGCAACAGATCCAGGAGCATTCACCTGCTCTCCAAACAGCCTTGTG 62

QY 231 CTTCACTACCTACCTCCCAACCTCCAGAGGGAGCAGCTATTTAAGGGAGCAGGAGTGAGAA 290
   |||||
Db 63 CTTCACTACCTACCTCCCAACCTCCAGAGGGAGCAGCTATTTAAGGGAGCAGGAGTGAGAA 122

QY 291 CAAACAGAGCGCTGGGATACAACTCTGGAGTCTCTGAG 332
   |||||
Db 123 CAAACAAGAGCGCTGGGATACAACTCTGGAGTCTCTGAG 164

RESULT 7
US-09-917-800A-1495
; Sequence 1495, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Blashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
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Query Match	25.4%	Score 84.4	DB 9	Length 3330
Best Local Similarity	64.9%	Pred. No. 1.2e-18		
Matches 157	Conservative	0	Mismatches 81	Indels 4
Gaps				
QY	67	CAAAACGCTGAAATGTTTGGCATCAGCTACTGACAGTAAGGTTTCCCAATCCTC	126	
Db	260	CGAAATCAGCTAAAGTTTATGATGGCCACAAACCCATGGTATGAGGGGCTTTCCGGGCCCTC	319	
QY	127	AACCTGTCTCGCAGCTGATGGGGAAGGAAGGATACCTAGGGGTATGG--CGA	184	
Db	320	AAGGCTGTCTCGCAGCTGTGGGGGGAAGGGGAAATTAACCAAGGCGTTGGGTATGC	379	
QY	185	CCAATCTGAGTCCACCAACTGACACAGCCCA--TCCCCAGCCTTGTGCCTACCTACCC	242	
Db	380	CCGCTCTGATCCATTATTGGCCACACCCACCTCCCATCTCTCGATCC	439	
QY	243	CCAACCTCCAGAGGAGCTATTTAAGGGAGCAGTTCAGACAAACAGACGG	302	
Db	440	CCAGCCCTCGAGAGGAAGACTATTAAAGAGCATTTGGGAGTACAGGAAAAACAAGGCAG	499	
QY	303	CC 304		
Db	500	GC 501		
RESULT 8				
US-10-152-319A-2157				
; Sequence 2157, Application US/10152319A				
; Publication No. US20040072160A1				
; GENERAL INFORMATION:				
; APPLICANT: Mendrick, Donna				
; APPLICANT: Porter, Mark				
; APPLICANT: Johnson, Kory				
; APPLICANT: Higgs, Brandon				
; APPLICANT: Castle, Arthur				
; APPLICANT: Elashoff, Michael				
; TITLE OF INVENTION: Molecular				
; FILE REFERENCE: 44921-5089-US				
; CURRENT APPLICATION NUMBER: US/10/152,319A				
; CURRENT FILING DATE: 2002-05-22				
; PRIOR APPLICATION NUMBER: US 60/292,335				
; PRIOR FILING DATE: 2001-05-22				
; PRIOR APPLICATION NUMBER: US 60/297,523				
; PRIOR FILING DATE: 2001-06-13				


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; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 398
; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 X51529
US-10-191-803-398

Query Match      25.4%; Score 84.4; DB 16; Length 3330;
Best Local Similarity 64.9%; Pred. No. 1.2e-18;
Matches 157; Conservative 0; Mismatches 81; Indels 4; Gaps 2;

QY 67 CAAAACCTGCTGAAATGTTTGGCATCAGCTACTGACACCGTAAGGTTTCCCAATCCTC 126
Db |||||
QY 127 AACTCTGCTCCAGCTGATGAGGGAGGAAAGGATTACTAGGGGTATGG--CGA 184
Db |||||
QY 320 AAGGCTGTTCTCCAGCTGTTGGGGGAAAGGGGAAATTACCCAGGGGTTGGGTATGC 379
Db |||||
QY 185 CCAATCTTGAGTCCCACTCAACCAAGCCCA--TCCCCAGCTTGTGCTCACTAACC 242
Db |||||
QY 380 CGTCTGTAATCCATTATTGGCCACACCCACCTCCCTGCTGCTCGATCC 439
Db |||||
QY 243 CCAACCTCCAGGAGGAGCAGCTATTTTAAGGGGAGCAGGTGCGAGCAACAAGACGG 302
Db |||||
QY 440 CCAGCCCTGCAGAGGAGAGCTATTTAAGAGCATTTGGGAGTACAGGAAACAAGCGAC 499
QY 303 CC 304
Db 500 GC 501

RESULT 10
US-09-925-300-70
; Sequence 70, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (911)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-70

Query Match      24.3%; Score 80.8; DB 9; Length 1076;
Best Local Similarity 95.3%; Pred. No. 1.4e-17;
Matches 82; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 247 CTCCAGAGGAGCAGCTATTTAAGGGAGCAGGATGCGAGAACAAACAAGCGCGTG 306
Db |||||
QY 2 CCAACAGAGGAGGAGCAGCTATTTAAGGGAGCAGGATGCGAGAACAAACAAGCGCGTG 61
QY 307 GGGATACAACTCTGGAGTCTCTGAG 332
```

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|||||
Db 62 GGGATACAACTCTGGAGTCTCTGAG 87

RESULT 11
US-09-981-353-17
; Sequence 17, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 474322.36
; NAME/KEY: unsure
; LOCATION: 388
; OTHER INFORMATION: a, t, c, g, or other
US-09-981-353-17

Query Match      15.1%; Score 50; DB 9; Length 735;
Best Local Similarity 100.0%; Pred. No. 8.7e-07;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 GTGCAGAACAAACAAGACGGCTGGGGATACAACTCTCGAGTCTCTGAG 332
Db |||||
QY 1 GTGCAGAACAAACAAGACGGCTGGGGATACAACTCTCGAGTCTCTGAG 50

RESULT 12
US-09-865-866-97
; Sequence 97, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 97
; LENGTH: 4990
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2026)...(2068)
; NAME/KEY: CDS
; LOCATION: (2245)...(2389)
; NAME/KEY: CDS
; LOCATION: (2622)...(2731)
; NAME/KEY: CDS
; LOCATION: (4098)...(4240)
US-09-865-866-97

Query Match      14.9%; Score 49.6; DB 10; Length 4990;
Best Local Similarity 59.4%; Pred. No. 2.8e-06;
Matches 139; Conservative 0; Mismatches 64; Indels 31; Gaps 2;

QY 67 CAAAACCTCCCTGAATGTGTTTGGCATCAGCTACTGACAGTAAAGGTTTCCCAATCCTC 126
Db |||||
QY 1016 CAAAATCAGCTGAATTTATGATGCGGCACCCCTTGTGTATGAAGGCTTTTCCAGCCCTC 1075
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Result No.	Score	Query Match	Length	DB	ID	Description	
1	33.8	10.2	420	4	US-09-547-435-17	Sequence 17, Appl	
2	33.8	10.2	1441	4	US-09-547-435-13	Sequence 13, Appl	
3	33.8	10.2	2236	4	US-09-547-435-5	Sequence 5, Appl	
4	33.8	10.2	2604	4	US-09-547-435-23	Sequence 23, Appl	
5	33.8	10.2	2701	4	US-09-547-435-1	Sequence 1, Appl	
6	33.8	10.2	3384	4	US-09-547-435-29	Sequence 29, Appl	
C 7	31.8	9.6	1036	4	US-09-205-258-86	Sequence 86, Appl	
C 8	30.6	9.2	305	3	US-09-328-111-618	Sequence 618, Appl	
C 9	30.6	9.2	2885	4	US-09-016-434-1143	Sequence 1143, Appl	
10	30.4	9.2	1549	2	US-08-856-448-1	Sequence 1, Appl	
11	30.2	9.1	340	4	US-09-833-381-1715	Sequence 1715, Ap	
12	30.2	9.1	1794	4	US-09-620-312D-988	Sequence 988, App	
C 13	29.6	8.9	9299	3	US-08-458-434A-7	Sequence 7, Appl	
14	29.4	8.9	1891	4	US-09-711-164-156	Sequence 156, App	
15	29.2	8.8	3111	2	US-09-014-969-12	Sequence 12, Appl	
C 16	29	8.7	204	4	US-09-506-729-37	Sequence 37, Appl	
C 17	29	8.7	455	4	US-09-623-976-2670	Sequence 2670, Ap	
C 18	29	8.7	1883	1	US-08-202-056-2	Sequence 2, Appl	
C 19	29	8.7	1933	1	US-08-076-093A-1	Sequence 1, Appl	
C 20	29	8.7	1933	1	US-08-410-451-1	Sequence 1, Appl	
C 21	29	8.7	1933	1	US-08-410-455-1	Sequence 1, Appl	
C 22	29	8.7	1933	1	US-08-418-919-1	Sequence 1, Appl	
C 23	29	8.7	1933	1	US-08-418-919-1	Sequence 1, Appl	
C 24	29	8.7	1933	1	US-08-410-453A-2	Sequence 2, Appl	
C 25	29	8.7	1933	1	US-08-703-255-1	Sequence 1, Appl	
C 26	29	8.7	1933	1	US-08-410-454A-2	Sequence 2, Appl	
C 27	29	8.7	1933	2	US-08-284-586-1	Sequence 1, Appl	
C	29	8.7	1933	2	US-08-410-456A-2	Sequence 2, Appl	

```

; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-547-435-13

Query Match      10.2%; Score 33.8; DB 4; Length 1441;
Best Local Similarity 53.4%; Pred. No. 0.12;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGTCCTGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGGCGACCAA 188
Db 492 CTCTGCCAGCAGCGTGTCTCAACAGTGGGCGAGCATGACTTTGGGGCCTGGATGCCCAA 551
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCTACCCCAACC 248
Db 552 TGCTCCATCATCCATGAGGAGCCCCACCCAGACCAAGGGGACCAACCCCTGAAGAC 611
QY 249 TCCCAGAGGGAGC 261
Db 612 TTACCTAGACACC 624

RESULT 3
US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-547-435-5

Query Match      10.2%; Score 33.8; DB 4; Length 2236;
Best Local Similarity 53.4%; Pred. No. 0.15;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGTCCTGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGGCGACCAA 188
Db 1287 CTCTGCCAGCAGCGTGTCTCAACAGTGGGCGAGCATGACTTTGGGGCCTGGATGCCCAA 1346
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCTACCCCAACC 248
Db 1347 TGCTCCATCATCCATGAGGAGCCCCACCCAGACCAAGGGGACCAACCCCTGAAGAC 1406
QY 249 TCCCAGAGGGAGC 261
Db 1407 TTACCTAGACACC 1419

RESULT 4
US-09-547-435-23
; Sequence 23, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2701
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-547-435-1

Query Match      10.2%; Score 33.8; DB 4; Length 2701;
Best Local Similarity 53.4%; Pred. No. 0.16;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGTCCTGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGGCGACCAA 188
Db 1752 CTCTGCCAGCAGCGTGTCTCAACAGTGGGCGAGCATGACTTTGGGGCCTGGATGCCCAA 1811
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCTACCCCAACC 248
Db 1812 TGCTCCATCATCCATGAGGAGCCCCACCCAGACCAAGGGGACCAACCCCTGAAGAC 1871
QY 249 TCCCAGAGGGAGC 261
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; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-547-435-13

Query Match      10.2%; Score 33.8; DB 4; Length 1441;
Best Local Similarity 53.4%; Pred. No. 0.12;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGTCCTGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGGCGACCAA 188
Db 492 CTCTGCCAGCAGCGTGTCTCAACAGTGGGCGAGCATGACTTTGGGGCCTGGATGCCCAA 551
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCTACCCCAACC 248
Db 552 TGCTCCATCATCCATGAGGAGCCCCACCCAGACCAAGGGGACCAACCCCTGAAGAC 611
QY 249 TCCCAGAGGGAGC 261
Db 612 TTACCTAGACACC 624

RESULT 3
US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-547-435-5

Query Match      10.2%; Score 33.8; DB 4; Length 2236;
Best Local Similarity 53.4%; Pred. No. 0.15;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGTCCTGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGGCGACCAA 188
Db 1287 CTCTGCCAGCAGCGTGTCTCAACAGTGGGCGAGCATGACTTTGGGGCCTGGATGCCCAA 1346
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCTACCCCAACC 248
Db 1347 TGCTCCATCATCCATGAGGAGCCCCACCCAGACCAAGGGGACCAACCCCTGAAGAC 1406
QY 249 TCCCAGAGGGAGC 261
Db 1407 TTACCTAGACACC 1419

RESULT 4
US-09-547-435-23
; Sequence 23, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2701
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-547-435-1

Query Match      10.2%; Score 33.8; DB 4; Length 2701;
Best Local Similarity 53.4%; Pred. No. 0.16;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 129 CTCTGTCCTGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGGGCGACCAA 188
Db 1752 CTCTGCCAGCAGCGTGTCTCAACAGTGGGCGAGCATGACTTTGGGGCCTGGATGCCCAA 1811
QY 189 TCCTGAGTCCCACTGACCAAGCCCATCCAGCCTTGTGCTCACTACCTACCCCAACC 248
Db 1812 TGCTCCATCATCCATGAGGAGCCCCACCCAGACCAAGGGGACCAACCCCTGAAGAC 1871
QY 249 TCCCAGAGGGAGC 261
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LOCATION: (1024)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (1032)
OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-86

Query Match
Best Local Similarity 9.6%; Score 31.8; DB 4; Length 1036;
Matches 69; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 189 TCTGTAGTCCACCACTGACACGCCCATCCCGAGCTTGTGCTACCTACCCCAACC 248
|||||
Db 852 TCTGTAGTCTCCACGCCCTGCGCCAGCCCTTCTGTGCTCTCCCGGCCCGCCAGGC 793
|||||

QY 249 TCCGAGGAGGAGCTATTAAAGGGAGGAGGAGTGCAGAACAAACAGAGCGCTGGG 308
|||||
Db 792 CAGGCGCTGGCGCAGCAATGCAATGCTGGGGTGGGATCACCAAGAGAGGCCAAGC 733
|||||

QY 309 GATACACTCT 319
|||||

Db 732 CAACTACCCCT 722
|||||

RESULT 8
US-09-328-111-618/c
Sequence 618, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER FILING DATE: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 618
LENGTH: 305
TYPE: DNA
ORGANISM: Homo sapiens
US-09-328-111-618

Query Match
Best Local Similarity 9.2%; Score 30.6; DB 3; Length 305;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 64 CGGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATC 123
|||||
Db 217 CGCCAAATAAACAGCATGTGTTGTAACATCCCCCAGTGGGGCTAGAAATCCCATG 158
|||||

QY 124 CTCACCTGTCTGCGAGCTGATGAGGGGAAGGAAGGA 164
|||||

Db 157 GTGACCTGTGACCTGCTCCCTGAGACAGGGGAGCCAGCA 117
|||||

RESULT 9
US-09-016-434-1143/c
Sequence 1143, Application US/09016434

Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1143:
SEQUENCE CHARACTERISTICS:
LENGTH: 2885 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1478280
US-09-016-434-1143

Query Match
Best Local Similarity 9.2%; Score 30.6; DB 4; Length 2885;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 64 CGGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATC 123
Db 2633 CGCCAAATAAACAGCATGTGTTGTAACATCCCCCAGTGGGGCTAGAAATCCCATG 2574
|||||

QY 124 CTCACCTGTCTGCGAGCTGATGAGGGGAAGGAAGGA 164
|||||

Db 2573 GTGACCTGTGACCTGCTCCCTGAGACAGGGGAGCCAGCA 2533
|||||

RESULT 10
US-08-856-444-1
Sequence 1, Application US/08856444
Patent No. 5959081
GENERAL INFORMATION:
APPLICANT: Lecka-Czernik, Beata
TITLE OF INVENTION: No. 5959081el Zinc Binding LIM Protein S2-6
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
ZIP: 77071
COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,444
FILING DATE: May 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5988
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1549 bp

TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: c-DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:

US-08-856-444-1

Query Match 9.2%; Score 30.4; DB 2; Length 1549;
Best Local Similarity 57.3%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 111 AGTTTCCCAATCCTCACTCTGCTCCAGCTGATGAGGGAAGGAAAGGGATTACCT 170
DB 530 AAGTGGCCCTCCGGCAGGCTGCTGCCAAGGAGGAGGGAAGCAGCAGGAAGCC 589
QY 171 AGGGGTATGGCGACCAATCCTGAGTCACCAACTG 206
DB 590 AGAGGGGCGAGAGCACTGCTGTACCACCAACGG 625

RESULT 11
US-09-833-381-1715
Sequence 1715, Application US/09833381
Patent No. 6672186
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1715
LENGTH: 340
TYPE: DNA
ORGANISM: Homo sapiens
US-09-833-381-1715

Query Match 9.1%; Score 30.2; DB 4; Length 340;
Best Local Similarity 62.7%; Pred. No. 0.96; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 132 TGTCCTCCAGCTGATGAGGGAAGGAAGGATTACTAGGGGTATGGGCGACCAATCC 191
DB 72 TGGCTTGCCTCCCAAGGAGGAGGGAAGCAGCAGGAAGAAAGCCAGAGGGGCGAGAGCACTGC 131
QY 192 TGAGTCCACCAACTG 206
DB 132 TGCTACCACCAACGG 146

RESULT 12
US-09-620-312D-988
Sequence 988, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt FL_genes Version 1.0
SEQ ID NO 988
LENGTH: 1794
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (164)..(1261)
US-09-620-312D-988

Query Match 9.1%; Score 30.2; DB 4; Length 1794;
Best Local Similarity 62.7%; Pred. No. 2.3; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 132 TGTCCTCCAGCTGATGAGGGAAGGAAGGATTACTAGGGGTATGGGCGACCAATCC 191
DB 778 TGGCTTGCCTCCCAAGGAGGAGGGAAGCAGCAGGAAGAAAGCCAGAGGGGCGAGAGCACTGC 837
QY 192 TGAGTCCACCAACTG 206
DB 838 TGCTACCACCAACGG 852

RESULT 13
US-08-458-434A-7/c
Sequence 7, Application US/08458434A
Patent No. 6083690
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Stephen E.
APPLICANT: Mundy M.D., Gregory R.
APPLICANT: Gosh-Choudhury Ph.D., Nandini
APPLICANT: Feng Ph.D., Jian Q.

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
;; TITLE OF INVENTION: OSTEOGENIC AGENTS
;; NUMBER OF SEQUENCES: 13
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: James C. Weseman, Esq.
;; STREET: 401 B. Street, Suite 1700
;; CITY: San Diego
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92101

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/458,434A

;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weseman, James C.
;; REGISTRATION NUMBER: 30,507
;; REFERENCE/DOCKET NUMBER: P00060US0
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 699-3604
;; TELEFAX: 619-236-1048

;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9299 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)

;; US-08-458-434A-7

Query Match 8.9%; Score 29.6; DB 3; Length 9299;
Best Local Similarity 59.5%; Pred. No. 9.1;
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 211 CGCCCATCCCGAGCTTGTGCTACCTACCCCACTCCAGAGGAGGAGTATTTA 270
DB 6318 CCCCCACCCCGCGCTTCTCGGCTCCAGCCCAATTCACAACTTCAGCTGGTTA 6259

QY 271 AGGGAGGAGGAGTGCAGAA 294
DB 6258 AGAACAGGAGGAGGAGAGACAGA 6235

RESULT 14
US-09-711-164-156
Sequence 156, Application US/09711164
Patent No. 6589738

GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith

TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF
FILE REFERENCE: ELITRA.008A

CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/164415

PRIOR FILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 156

LENGTH: 891
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(891)

US-09-711-164-156

Query Match 8.9%; Score 29.4; DB 4; Length 891;
Best Local Similarity 56.8%; Pred. No. 3;
Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 52 CAAATTCGACGCGGCAAACTGCCTGAAATGTGTTTGGCATCAGCTACTGACACGTAA 111
DB 751 CAATACCTCAACCGCAAACTACCTGTGGGGTGACTTTGCCGCGCTGCGGTGATGTCT 810

QY 112 GGTTCCTCAATCTCAACTCTGTCTGCCAGCTGA 146
DB 811 GCATTACGATCACCATCGTCTTCTTGTGCTCA 845

RESULT 15
US-09-014-969-12

Sequence 12, Application US/09014969
Patent No. 5965397
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3111 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-09-014-969-12

Query Match 8.8%; Score 29.2; DB 2; Length 3111;
Best Local Similarity 57.8%; Pred. No. 7;
Matches 52; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 133 GTCCTGCCAGCTGATCAGGGGAGGAAAGGATTACCTAGGGGTATGGCGGACCAATCCT 192
DB 957 GTCGTCCCGGCTGATCAGCAGCTTGAGATAGAAAGACTACAGGTGAGCTGTCCAAATCCC 1016

QY 193 GAGTCCACCACTGACACGCGCCATCCCA 222
DB 1017 CATGCGGGATCTTCCACACCGCTCTCA 1046

Search completed: September 11, 2004, 09:33:15
Job time : 52.2049 secs

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 09:20:47 ; Search time 262.86 Seconds
(without alignments)
5187.326 Million cell updates/sec

Title: US-09-808-388-5

Perfect score: 271

Sequence: 1 cgcggcaaaactgctgaaa.....caactctggagctctctgag 271

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	271	100.0	271	9	US-09-808-388-5
2	271	100.0	332	9	US-09-808-388-6
3	212	78.2	1080	10	US-09-865-866-17
4	164.2	60.6	6083	13	US-10-221-714A-440
5	150.2	55.4	6083	13	US-10-221-714A-439
6	118.8	43.8	967	15	US-10-210-120-75
7	84.4	31.1	3330	9	US-09-917-800A-1495
8	84.4	31.1	3330	12	US-10-152-319A-2157
9	84.4	31.1	3330	16	US-10-191-803-398
10	80.8	29.8	1076	9	US-09-925-300-70
11	50	18.5	735	9	US-09-981-353-17
12	49.6	18.3	4990	10	US-09-865-866-97
13	34.2	12.6	371	15	US-10-387-495-8
14	34.2	12.6	742	13	US-10-027-632-151276

C	15	34.2	12.6	742	16	US-10-027-632-151276
	16	33.8	12.5	420	15	US-10-422-264-17
	17	33.8	12.5	1441	15	US-10-422-264-13
	18	33.8	12.5	2136	9	US-09-862-658-3
	19	33.8	12.5	2136	15	US-10-175-596-24
	20	33.8	12.5	2136	17	US-10-776-871-24
	21	33.8	12.5	2236	15	US-10-422-264-5
	22	33.8	12.5	2307	13	US-10-302-172-803
	23	33.8	12.5	2604	15	US-10-422-264-23
	24	33.8	12.5	2701	15	US-10-422-264-1
	25	33.8	12.5	3320	9	US-09-862-658-1
	26	33.8	12.5	3320	15	US-10-175-596-22
	27	33.8	12.5	3320	17	US-10-776-871-22
	28	33.8	12.5	3384	15	US-10-422-264-29
	29	33.2	12.3	2835	16	US-10-104-047-1501
	30	32.6	12.0	54552	13	US-10-087-192-1303
C	31	32.4	12.0	819	13	US-10-027-632-130312
	32	32.4	12.0	819	16	US-10-027-632-130312
	33	32.4	12.0	94529	16	US-10-034-650-52
	34	32.2	11.9	573	13	US-10-027-632-50048
	35	32.2	11.9	573	13	US-10-027-632-50049
	36	32.2	11.9	573	13	US-10-027-632-69880
	37	32.2	11.9	573	13	US-10-027-632-69881
	38	32.2	11.9	573	13	US-10-027-632-70565
	39	32.2	11.9	573	13	US-10-027-632-70566
	40	32.2	11.9	573	16	US-10-027-632-50048
	41	32.2	11.9	573	16	US-10-027-632-50049
	42	32.2	11.9	573	16	US-10-027-632-69880
	43	32.2	11.9	573	16	US-10-027-632-69881
	44	32.2	11.9	573	16	US-10-027-632-70565
	45	32.2	11.9	573	16	US-10-027-632-70566

ALIGNMENTS

RESULT 1
US-09-808-388-5
; Sequence 5, Application US/09/808,388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment of the PLA2s promoter
US-09-808-388-5

Query Match 100.0%; Score 271; DB 9; Length 271;

Best Local Similarity 100.0%; Pred. No. 1.5e-85;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCAAAACTGCTGAAATGTTTGGCATCAGTACTGACGTAAGTTTCCCAA 60

Db 1 CGCGCAAAACTGCTGAAATGTTTGGCATCAGTACTGACGTAAGTTTCCCAA 60

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QY 61 TCCTCAACTCTGCTCTGCCAGCTGATAGGGGAAGAAAGGGATTACCTAGGGGTATGGG 120
Db 61 TCCTCAACTCTGCTCTGCCAGCTGATAGGGGAAGAAAGGGATTACCTAGGGGTATGGG 120
QY 121 CGACCAATCTCTGAGTCCACCACTGACCAAGCCCATCCCGAGCCTTGCGCTCACTTACC 180
Db 121 CGACCAATCTCTGAGTCCACCACTGACCAAGCCCATCCCGAGCCTTGCGCTCACTTACC 180
QY 181 CCCAACCTCCAGAGGAGCAGCTATTAAAGGGGAGCAGGAGTGCAGAACAAACAAGACG 240
Db 181 CCCAACCTCCAGAGGAGCAGCTATTAAAGGGGAGCAGGAGTGCAGAACAAACAAGACG 240
QY 241 GCCTGGGGATACAACTCTGGAGTCTCTGAG 271
Db 241 GCCTGGGGATACAACTCTGGAGTCTCTGAG 271

RESULT 2
US-09-808-388-6
; Sequence 6, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massead, Charbel
; APPLICANT: Berendaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Collette
; APPLICANT: Berezziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 332
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE/PLA2s hybrid promoter
US-09-808-388-6

Query Match 100.0%; Score 271; DB 9; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.6e-85;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGGCAAAACTGCTGAAATGTTTGGCATCAGTACGTACGTACGTAAGGTTTCCCAA 60
Db 62 CGCGGCAAAACTGCTGAAATGTTTGGCATCAGTACGTACGTACGTAAGGTTTCCCAA 121
QY 61 TCCTCAACTCTGCTCTGCCAGCTGATAGGGGAAGAAAGGGATTACCTAGGGGTATGGG 120
Db 122 TCCTCAACTCTGCTCTGCCAGCTGATAGGGGAAGAAAGGGATTACCTAGGGGTATGGG 181
QY 121 CGACCAATCTCTGAGTCCACCACTGACCAAGCCCATCCCGAGCCTTGCGCTCACTTACC 180
Db 182 CGACCAATCTCTGAGTCCACCACTGACCAAGCCCATCCCGAGCCTTGCGCTCACTTACC 241
QY 181 CCCAACCTCCAGAGGAGCAGCTATTAAAGGGGAGCAGGAGTGCAGAACAAACAAGACG 240
Db 242 CCCAACCTCCAGAGGAGCAGCTATTAAAGGGGAGCAGGAGTGCAGAACAAACAAGACG 301
QY 241 GCCTGGGGATACAACTCTGGAGTCTCTGAG 271
Db 302 GCCTGGGGATACAACTCTGGAGTCTCTGAG 332

RESULT 3
US-09-865-866-17
; Sequence 17, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXPL
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 17
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-865-866-17

Query Match 78.2%; Score 212; DB 10; Length 1080;
Best Local Similarity 93.1%; Pred. No. 1.9e-64;
Matches 255; Conservative 0; Mismatches 15; Indels 4; Gaps 3;
QY 1 CGCGCAAAACTGCTGAAATGTTTGGCATCAGTACGTACGTAAGGTTTCCCAA 59
Db 763 CTGCGCAAAACTGCTGAAATGTTTGGCATCAGTACGTACGTAAGGTTTCCCAA 822
QY 60 ATCCTCAACTCTGCTCTG-CCAGCTGATAGGGGAAGAAAGGGATTACCTAGGGGTAT 117
Db 823 ATCCTCAACTCTGCTCTGCTGCCAGGCTGATAGGGGAAGAAAGGGATTACCTAGGGGTAT 882
QY 118 GGGCGACCAATCCTGAGTCCCACTGACCACTGACCACTGCCAGCTTGTGCTCACCT 177
Db 883 GGGCGACCAATCCTGAGTCCCACTGACCACTGCCAGCTTGTGCTCACCT 942
QY 178 ACCCCCACTCCAGAGGAGCAGCTATTAAAGGGGAGCAGGAGTGCAGAACAAACAAG 237
Db 943 ACCCCCACT-CCAGAGGAGCAGCTATTAAAGGGGAGCAGGAGTGCAGAACAAACAAG 1001
QY 238 ACGGCTGGGGATACAACTCTGGAGTCTCTGAG 271
Db 1002 ACGGCTGGGGATACAACTCTGGAGTCTCTGAG 1035

RESULT 4
US-10-221-714A-440/c
; Sequence 440, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 440
; LENGTH: 6083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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```
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-440

Query Match      60.6%; Score 164.2; DB 13; Length 6083;
Best Local Similarity 76.2%; Pred. No. 2.8e-47;
Matches 202; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY      6 CAAACTGCGCTGAAATGTTTGGCATCAGCTACTGACAGTAAAGTTTCCCAATCCTC 65
Db      1324 CAAAACACTACCTAAATATATTTTAAACATCAACTACTAACAGTAAAAATTTCCCAATCCTC 1265

QY      66 AACTCTGTCTGCCAGCTGATGAGGGAAGAAAGGATTACCTAGGGGTATGGCGACC 125
Db      1264 AACTCTATCTTACCACCTAATAAAAAAATAAAAAAATTAACCTAAAAATAAACGACC 1205

QY      126 AATCCTGAGTCCCAACTGACACGCGCCATCCCGCCTTGTGCTCCTACCTACCCCAA 185
Db      1204 AATCCTAAATCCCACTAACTAACCAAGCCCATCCCACTTATACCTCACTACCCCAA 1145

QY      186 CCTCCGAGAGGAGCAGCTATTTAAGGGGAGCAGAGTGCAGAACAAACAGAGCGCTG 245
Db      1144 CTTCCCAAAAAAACAACACTATTTTAAAAAACAACAAAAATACAAAAACAACAAACGACCTA 1085

QY      246 GGGATACAACTCTGGAGTCTCTGA 270
Db      1084 AAAATACAACTTAATAATCTCTTAA 1060

RESULT 5
US-10-221-714A-439
; Sequence 439, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221.714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 439
; LENGTH: 6083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-439

Query Match      55.4%; Score 150.2; DB 13; Length 6083;
Best Local Similarity 72.7%; Pred. No. 2.6e-42;
Matches 194; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY      5 GCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACCTAAGTTTCCCAATCCT 64
Db      4759 GTAAATGTTGAAATGTTTGGTATTAGTTATTGATACGTAAGGTTTCTTAATTTT 4818

QY      65 CAATCTGTCTGCTGACGCTGATGAGGGAAGGAAAGGATTACCTAGGGGTATGGCGAC 124
Db      4819 TAATTTTGTGTTTGTAGTTGATGAGGGAAGGAAAGGATTATTAGGGGTATGGGCGAT 4878
```

```
QY      125 CAATCTGAGTCCCAACTGACCAAGCCCATCCCGCCTTGTGCTCCTACCTACCCCA 184
Db      4879 TAATTTTGGATTATTAATTGATTACGTTTATTTTAGTTTGTGTTTATTTATTTT 4938

QY      185 ACCTCCAGAGGGAGCAGCTATTTAAGGGAGCAGGAGTGCAGAACAAACAGCGCCT 244
Db      4939 ATTTTGTAGGGAGTAGTTATTTAAGGGAGTAGGAGTGTAGAAATAATAAGACGGTTT 4998

QY      245 GGGATACAACTCTGGAGTCTCTGAG 271
Db      4999 GGGATATATTTTGGAGTTTGTGAG 5025

RESULT 6
US-10-210-120-75
; Sequence 75, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210.120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 967
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-75

Query Match      43.8%; Score 118.8; DB 15; Length 967;
Best Local Similarity 83.3%; Pred. No. 1.9e-31;
Matches 135; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY      110 AGGGTATGGGCGACCAATCCTGAGTCCCACTGACCACTGACAGGCCATCCCGAGCCTTGTG 169
Db      3 AGGAAAAAGAGCAACAGATCCAGGAGCATTCACCTGCCCTGTCTCCAAACAGCCTTGTG 62

QY      170 CCTCACCTACCCCAACCTCCAGAGGGAGCAGCTATTTAAGGGGAGCAGAGTGCAGAA 229
Db      63 CCTCACCTACCCCAACCTCCAGAGGGAGCAGCTATTTAAGGGGAGCAGAGTGCAGAA 122

QY      230 CAAACAGACGGCTGGGATACAACTCTGGAGTCTCTGAG 271
Db      123 CAAACAGACGGCTGGGATACAACTCTGGAGTCTCTGAG 164

RESULT 7
US-09-917-800A-1495
; Sequence 1495, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castile, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
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; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1495
; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 X51529
US-09-917-800A-1495

Query Match 31.1%; Score 84.4; DB 9; Length 3330;
Best Local Similarity 64.9%; Pred. No. 4.4e-19;
Matches 157; Conservative 0; Mismatches 81; Indels 4; Gaps 2;
QY 6 CAAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCTC 65
DB 260 CCAATCAGCTAAAGTTTATGATGCGCAACCCATGGTATGAGGGCTTTCCGGCCCTC 319
QY 66 AACTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGG--CGA 123
DB 320 AAGGCTGTTCTGCCAGCTGTTGGGGGAAAGGGGAAATACCCAGGGGGTGGGTATGC 379
QY 124 CCAATCTGTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGG--CGA 181
DB 380 CGGCTGTGTAATCCATTATTTGGCCACACCCACCTCCCATCCCTGTGGCTCTCCGATCC 439
QY 182 CCAACTCTCCAGAGGAGCAGCTATTTAAGGGGAGCAGAGTGCGAGAAACAAACAGACGG 241
DB 440 CCAGCCCTCCAGAGGAGAGCTATTTAAGAGCATTTGGAGTACAGGAAACAGGCAG 499
QY 242 CC 243
DB 500 GC 501

RESULT 8
US-10-152-319A-2157
; Sequence 2157, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5099-US
; CURRENT APPLICATION NUMBER: US/10/152,319A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2157
; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X51529
US-10-152-319A-2157

Query Match 31.1%; Score 84.4; DB 12; Length 3330;
Best Local Similarity 64.9%; Pred. No. 4.4e-19;
Matches 157; Conservative 0; Mismatches 81; Indels 4; Gaps 2;
QY 6 CAAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCTC 65
DB 260 CCAATCAGCTAAAGTTTATGATGCGCAACCCATGGTATGAGGGCTTTCCGGCCCTC 319
QY 66 AACTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGG--CGA 123
DB 320 AAGGCTGTTCTGCCAGCTGTTGGGGGAAAGGGGAAATACCCAGGGGGTGGGTATGC 379
QY 124 CCAATCTGTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGG--CGA 181
DB 380 CGGCTGTGTAATCCATTATTTGGCCACACCCACCTCCCATCCCTGTGGCTCTCCGATCC 439
QY 182 CCAACTCTCCAGAGGAGCAGCTATTTAAGGGGAGCAGAGTGCGAGAAACAAACAGACGG 241
DB 440 CCAGCCCTCCAGAGGAGAGCTATTTAAGAGCATTTGGAGTACAGGAAACAAAGGCAG 499
QY 242 CC 243
DB 500 GC 501

RESULT 9
US-10-191-803-398
; Sequence 398, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 398
; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 X51529
US-10-191-803-398

Query Match      31.1%; Score 84.4; DB 16; Length 3330;
Best Local Similarity 64.9%; Pred. No. 4.4e-19;
Matches 157; Conservative 0; Mismatches 81; Indels 4; Gaps 2;

QY      6 CAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCTC 65
Db      260 CGAAATCAGCTAAAGTTTATGATGGCCACACCCATGATGAGGGCTTTTCGGGCCCTC 319

QY      66 AACTCTGCTGCTGCAGCTGATGAGGGGAAGGAAGGATTACCTAGGGGTATGG--CGA 123
Db      320 AAGGCTGTTCTGCCAGCTGTTGGGGGAAAGGGGAATTTACCAGGGCGTTGGGTATGC 379

QY      124 CCAATCTGAGTCACCAACTGACACCGCCA--TCCCCAGCCTTGTGCTCCTACCTACCC 181
Db      380 CCGTCTGTGAATCCATTATTATTGGCCACACCCACCTCCCCCATCCCTGTGCTCTCCGATCC 439

QY      182 CCACCTCCAGAGGAGCAGCTATTAAAGGGAGCAGGAGTGCAGAACAAACAGACGG 241
Db      440 CCAGCCTCGCAGAGGGAAGAGCTATTTTAGAGCATTTGGGAGTACAGGAAAAACAGGCAG 499

QY      242 CC 243
Db      500 GC 501

RESULT 10
US-09-925-300-70
; Sequence 70, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR APPLICATION DATE: 2001-08-10
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 1999-03-12
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (911)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-70

Query Match      29.8%; Score 80.8; DB 9; Length 1076;
Best Local Similarity 95.3%; Pred. No. 5.8e-18;
Matches 82; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      186 CTTCCAGAGGAGCAGCTATTTAAGGGAGCAGGAGTGCAGAACAAACAGAGCGGCTG 245
Db      2 CCAACAGAGGAGCAGCTATTTAAGGGAGCAGGAGTGCAGAACAAACAGAGCGGCTG 61

QY      246 GGGATACAACTCTGGAGTCTCTGAG 271
Db      62 GGGATACAACTCTGGAGTCTCTGAG 87
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RESULT 11
US-09-981-353-17
; Sequence 17, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 474322.36
; NAME/KEY: unsure
; LOCATION: 388
; OTHER INFORMATION: a, t, c, g, or other
US-09-981-353-17

Query Match      18.5%; Score 50; DB 9; Length 735;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      222 GTGAGAACAAACAGACGGCCTGGGATACAACTCTGGAGTCTCTGAG 271
Db      1 GTGAGAACAAACAGACGGCCTGGGATACAACTCTGGAGTCTCTGAG 50

RESULT 12
US-09-865-866-97
; Sequence 97, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXH
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 97
; LENGTH: 4990
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2026)...(2068)
; NAME/KEY: CDS
; LOCATION: (2245)...(2389)
; NAME/KEY: CDS
; LOCATION: (2622)...(2731)
; NAME/KEY: CDS
; LOCATION: (4098)...(4240)
US-09-865-866-97

Query Match      18.3%; Score 49.6; DB 10; Length 4990;
Best Local Similarity 59.4%; Pred. No. 1.1e-06;
Matches 139; Conservative 0; Mismatches 64; Indels 31; Gaps 2;

QY      6 CAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCTC 65
Db      1016 CAAATCAGCTGAAATTTATGATGGCGCACCCCTTGGTATGAGGCTTTTCAGGCCCTC 1075

QY      66 AACTCTGTCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGGCGACC 125
Db      1076 AGGGCTGCCCTGCCAGCTGTTGGGGAACAAAAGGCCATTGGGTATGC-----CC 1125
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Qy	126	AATCCTGAGTCCACCAACTGACGACGCGCATCCCGACGCTTGTCCTCACTACCCCCAA	185
Db	1126	ATCGTGAATCCCATTTTGACCAACCCACCT-----CCCAT	1164
Qy	186	CCTCCGAGGGGACGACGCTATTTTAAGGGGAGCAGAGTGCAGAACAAACAGAC	239
Db	1165	CCCTGCAGAGGGAAGAGCTATTTAAGGGCACTTGCATTCAGGAAAACCAAGAC	1218

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RESULT 13
US-10-387-495-8/c
; Sequence 8, Application US/10387495
; Publication No. US20030162956A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Leukocyte Regulatory Factors 1 and 2
; FILE REFERENCE: PE359C1
; CURRENT APPLICATION NUMBER: US/10/387,495
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/09/603,735A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 03/055,998
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/043,483
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-387-495-8

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	Query Match	12.6%	Score 34.2	DB 15	Length 371
	Best Local Similarity	51.7%	Pred. No. 0.14		
	Matches	78	Conservative 0	Mismatches 73	Indels 0
	Gaps	0			
Qy	23	TGTTTTGGCATCAGTACTGACAGTAAAGGTTTCCCAATCCTCAACTCTGTCCTGCCAGC	82		
Db	238	TGTTGGGACACAGCCCGAGGTCAGGTAGGAGTGCCTCCTCAAAATCTCTCCACCCCC	179		
Qy	83	TGATGAGGGGAGGAAAGGGATTACCTAGGGGTATGGCGACCAATCTGAGTCCACAA	142		
Db	178	AGGACTCAGGAGGAGGGCAGGAGAGGTGTGGCCCGGTGTGACGTCTCAGGGGGCTC	119		
Qy	143	CTGACACGCCCCATCCCCAGCCTTTGTGCCTC	173		
Db	118	CTGAGCTCGAGCCACACGAGCCTTTGTGCCTC	88		

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RESULT 14
US-10-027-632-151276/c
; Sequence 151276, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

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; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151276
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-151276

Query Match          12.6%; Score 34.2; DB 13; Length 742;
Best Local Similarity 53.3%; Pred. No. 0.17;
Matches 72; Conservative 0; Mismatches 63; Indels 0; Gaps 0

Qy      56  CCCAATCCTCAACTCTCTCTGCCAGCTGTATGAGGGGAAGAAAGGATTAACCTAGGGGT 115
      |||||
Db      489  CCCAAACCCCAAGGAAGCCCTAACAGTTGCTGAGCAGAGGGAAGCTGCTCCATAGGCG 430

Qy      116  ATGGGGACCAATCCTGAGTCCCACTGACACAGGCCATCCCCAGCCTGTGTGCTCAC 175
      |||||
Db      429  GTGGGCCCATCGTTTCTCAGTCCCAAGCAAGAGGAGTCAATGGTCCCCACAGCCACA 370
      |||||

Qy      176  CTACCCCCCAACCTCC 190
      |||||
Db      369  GCATCTCCAAACCCCC 355

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RESULT 15
US-10-027-632-151276/c
; Sequence 151276, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151276
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-151276

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	Query Match	12.6%	Score 34.2;	DB 16;	Length 742;
	Best Local Similarity	53.3%;	Pred. No. 0.17;		
Matches	72;	Conservative 0;	Mismatches 63;	Indels 0;	Gaps 0;
Qy	56	CCCAATCTCAACTCTGTCTGTCAGCTGATGAGGGGAAGAAAGGANTTACCTAGGGGT	115		
Dd	489	CCCAAAACCAGAAAGGCCTAACAGTTGCTGACGAGAGGAAGCTCTCCATAGGGCG	430		
Qy	116	ATGGGCGACCAANTCCTAGTGCCCAACTGACCAAGCCCCCATCCCAGAGCTTGTGGCTCAC	175		
Dd	429	GTGGGCCCATCGTTTCTCAGTCCCCCAAAGAGAGGTCTAGGTCCTCCCCCAGGCCACA	370		
Ov	176	CTACCCCCCAACCTCC	190		

Db 369 GCATCTCCAAACCCC 355

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Job time : 263.86 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-808-388-5

Perfect score: 271

Sequence: 1 cgcggcaaaactgcctgaaa.....caactctggagctctctgag 271

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	33.8	12.5	420	US-09-547-435-17	Sequence 17, Appl
2	33.8	12.5	1441	US-09-547-435-13	Sequence 13, Appl
3	33.8	12.5	2236	US-09-547-435-5	Sequence 5, Appl
4	33.8	12.5	2604	US-09-547-435-23	Sequence 23, Appl
5	33.8	12.5	2701	US-09-547-435-1	Sequence 1, Appl
6	33.8	12.5	3384	US-09-547-435-29	Sequence 29, Appl
7	31.8	11.7	1036	US-09-205-258-86	Sequence 86, Appl
8	30.6	11.3	305	US-09-328-111-618	Sequence 618, App
9	30.6	11.3	2885	US-09-016-434-1143	Sequence 1143, Ap
10	30.4	11.2	1549	US-08-856-444-1	Sequence 1, Appl
11	30.2	11.1	340	US-09-833-381-1715	Sequence 1715, Ap
12	30.2	11.1	1794	US-09-820-312D-988	Sequence 988, App
13	29.6	10.9	9299	US-08-458-434A-7	Sequence 7, Appl
14	29.2	10.8	3111	US-09-014-969-12	Sequence 12, Appl
15	29	10.7	204	US-09-506-729-37	Sequence 37, Appl
16	29	10.7	455	US-09-621-976-2670	Sequence 2670, Ap
17	29	10.7	1883	US-08-202-056-2	Sequence 2, Appl
18	29	10.7	1933	US-08-076-093A-1	Sequence 1, Appl
19	29	10.7	1933	US-08-410-451-1	Sequence 1, Appl
20	29	10.7	1933	US-08-410-455-1	Sequence 1, Appl
21	29	10.7	1933	US-08-418-919-1	Sequence 1, Appl
22	29	10.7	1933	US-08-410-453A-2	Sequence 2, Appl
23	29	10.7	1933	US-08-701-265-1	Sequence 1, Appl
24	29	10.7	1933	US-08-410-454A-2	Sequence 2, Appl
25	29	10.7	1933	US-08-284-586-1	Sequence 1, Appl
26	29	10.7	1933	US-08-410-456A-2	Sequence 2, Appl
27	29	10.7	1933	US-08-805-478-1	Sequence 1, Appl

C 28	29	10.7	1933	2	US-08-802-627A-1	Sequence 1, Appli
C 29	29	10.7	1933	2	US-08-801-238-1	Sequence 1, Appli
C 30	29	10.7	1933	2	US-08-801-228-1	Sequence 1, Appli
C 31	29	10.7	1933	3	US-09-104-296-1	Sequence 1, Appli
C 32	29	10.7	1933	4	US-09-023-655-1134	Sequence 1134, Ap
C 33	29	10.7	1933	5	PCT-US94-06380-1	Sequence 1, Appli
C 34	28.8	10.6	231	4	US-09-023-655-321	Sequence 321, App
C 35	28.6	10.6	891	4	US-09-711-164-156	Sequence 156, App
C 36	28.6	10.6	3728	1	US-08-111-939-1	Sequence 1, Appli
C 37	28.4	10.5	501	4	US-09-252-991A-1881	Sequence 1881, Ap
C 38	28.4	10.5	666	4	US-09-252-991A-2156	Sequence 2156, Ap
C 39	28.4	10.5	708	4	US-09-252-991A-1729	Sequence 1729, Ap
C 40	28.4	10.5	897	4	US-09-252-991A-2083	Sequence 2083, Ap
C 41	28.4	10.5	1119	4	US-09-252-991A-1806	Sequence 1806, Ap
C 42	28.4	10.5	2992	4	US-09-362-123A-3	Sequence 306, App
C 43	28.4	10.5	9053	4	US-09-976-594-306	Sequence 306, App
C 44	28.2	10.4	33	1	US-08-186-895-4	Sequence 4, Appli
C 45	28.2	10.4	452	4	US-09-702-705-829	Sequence 829, App

ALIGNMENTS

RESULT 1
US-09-547-435-17
; Sequence 17, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-17

Query Match	12.5%	Score 33.8	DB 4	Length 420
Best Local Similarity	53.4%	Pred. No. 0.081		
Matches	71	Conservative	0	Mismatches 62; Indels 0; Gaps 0
QY	68	CTCTGTCCTGCCAGCTGATGAGGGGAAGGAAGGGATTACTAGGGGTATGGGCGACCAA	127	
Db	36	CTCTGCCAGCAGCTGCTGTCAACAGTGGGAGCATGACTTTGGGCGCTGGATGCCAA	95	
QY	128	TCTGTAGTCCCACTACACAGCCCTCCAGCCCTGTGCTGTGCTACCTACCTACCTACCTACCT	187	
Db	96	TGCTCCATCATCATGAGGAGCCGCCCCAGAGACCAAGGGGACCAACCTCTGAAGAC	155	
QY	188	TCCAGAGGGAGC	200	
Db	156	TTACCTAGACACC	168	

RESULT 2
US-09-547-435-13
; Sequence 13, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.

```

; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-13

Query Match      12.5%; Score 33.8; DB 4; Length 1441;
Best Local Similarity 53.4%; Pred. No. 0.14;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 68 CTCTGTCTGCCAGCTGATGAGGGGAAGGATTACCTAGGGGTATGGCGACCAA 127
Db 492 CTCTGCCAGACCGTCTGCTCAACAGTGGCAGCATGACTTTGGGGCTGGATGCCCAA 551
QY 128 TCCTGAGTCCCAACTGACCAACGCCCATCCCCAGCCTTGTGCTCTCACTACCCCAACC 187
Db 552 TGCTCCATCATCCATGAGGAGCCCCACCCAGACCAAGGGGACCAACCCCTGAAGAC 611
QY 188 TCCCAGAGGGAGC 200
Db 612 TTACCTAGACACC 624

RESULT 3
US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-5

Query Match      12.5%; Score 33.8; DB 4; Length 2236;
Best Local Similarity 53.4%; Pred. No. 0.17;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 68 CTCTGTCTGCCAGCTGATGAGGGGAAGGATTACCTAGGGGTATGGCGACCAA 127
Db 1287 CTCTGCCAGACCGTCTGCTCAACAGTGGCAGCATGACTTTGGGGCTGGATGCCCAA 1346
QY 128 TCCTGAGTCCCAACTGACCAACGCCCATCCCCAGCCTTGTGCTCTCACTACCCCAACC 187
Db 1347 TGCTCCATCATCCATGAGGAGCCCCACCCAGACCAAGGGGACCAACCCCTGAAGAC 1406
QY 188 TCCCAGAGGGAGC 200
Db 1407 TTACCTAGACACC 1419

RESULT 4
US-09-547-435-23
; Sequence 23, Application US/09547435
; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2701
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-547-435-1

Query Match      12.5%; Score 33.8; DB 4; Length 2701;
Best Local Similarity 53.4%; Pred. No. 0.18;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 68 CTCTGTCTGCCAGCTGATGAGGGGAAGGATTACCTAGGGGTATGGCGACCAA 127
Db 1752 CTCTGCCAGACCGTCTGCTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCCAA 1811
QY 128 TCCTGAGTCCCAACTGACCAACGCCCATCCCCAGCCTTGTGCTCTCACTACCCCAACC 187
Db 1812 TGCTCCATCATCCATGAGGAGCCCCACCCAGACCAAGGGGACCAACCCCTGAAGAC 1871
QY 188 TCCCAGAGGGAGC 200
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Db	1872	TTACCTAGACACC	1884
RESULT 6			
US-09-547-435-29			
; Sequence 29, Application US/09547435			
; Patent No. 6582957			
; GENERAL INFORMATION:			
; APPLICANT: Turner, C. Alexander, Jr.			
; APPLICANT: Zambrowicz, Brian			
; APPLICANT: Nehls, Michael			
; APPLICANT: Friedrich, Glenn			
; APPLICANT: Sands, Arthur T.			
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides			
; FILE REFERENCE: 7705.0009-00000			
; CURRENT APPLICATION NUMBER: US/09/547,435			
; CURRENT FILING DATE: 2000-04-12			
; NUMBER OF SEQ ID NOS: 29			
; SOFTWARE: Fast-SEQ for Windows Version 3.0			
; SEQ ID NO 29			
; LENGTH: 3384			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-547-435-29			
Query Match	12.5%	Score 33.8;	DB 4; Length 3384;
Best Local Similarity	53.4%	Pred. No. 0.2;	
Matches	71;	Conservative	0; Mismatches 62; Indels 0; Gaps 0;
QY	68	CTCTGTCCTGCCAGCTGATGAGGGGAAGAAAGGATTACTTAGGGGTATGGGGACCAA	127
Db	2250	CTCTGCCACGACGCTGCTCTCAACATGGGCGAGCATGACTTTGGGGCCCTGGATGCCAA	2309
QY	128	TCTGTAGTCACCACTGACACGCCCATCCCGAGCCCTTGTGCTTACCTTACCCCAACC	187
Db	2310	TGTCCTCATCTCATGAGCGAGCGCCCAACCCAGACCAAGGGGACCACTCTGAGAC	2369
QY	188	TCCACAGGGGAC	200
Db	2370	TTACCTAGACACC	2382
RESULT 7			
US-09-205-258-86/c			
; Sequence 86, Application US/09205258			
; Patent No. 6525174			
; GENERAL INFORMATION:			
; APPLICANT: Young et al.			
; TITLE OF INVENTION: 207 Human Secreted Proteins			
; FILE REFERENCE: PZ007P1			
; CURRENT APPLICATION NUMBER: US/09/205,258			
; CURRENT FILING DATE: 1998-12-04			
; EARLIER APPLICATION NUMBER: PCT/US98/11422			
; EARLIER FILING DATE: 1998-06-04			
; EARLIER APPLICATION NUMBER: 60/048,885			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/049,375			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,881			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,880			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,896			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/049,020			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,876			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,895			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,884			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,894			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,971			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,964			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,882			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,899			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,893			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,900			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,901			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,892			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,915			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/049,019			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,970			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,972			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,916			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/049,373			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,875			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/049,374			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,917			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,949			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,974			
; EARLIER FILING DATE: 1997-06-06			
; EARLIER APPLICATION NUMBER: 60/048,883			
; EARLIER FILING DATE: 1997-06-06			

Mon Sep 13 07:48:10 2004

us-09-808-388-5.sept04.rni

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; LOCATION: (1024)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1032)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-86

Query Match      11.7%; Score 31.8; DB 4; Length 1036;
Best Local Similarity 52.7%; Pred. No. 0.57;
Matches 69; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 128 TCCTGAGTCCACCAACTGACCAACCCATCCCGAGCCTTTGCGCTACCTACCCCAACC 187
Db 852 TCCTGAGTCCACCGCCCTGCGAGCCCTTCTGCTGCTCTCCCGCGCCCGCCAGGC 793

Qy 188 TCCGAGAGGGAGCGAGCTATTTAAGGGAGCAGGAGTGCAGAACAAACAGACGCGCTGG 247
Db 792 CAGGCGCTGGCGAGCAATGCAATGGCTGGGGGTGGGATCACCAGAGAGAGGCCAAGC 733

Qy 248 GATACAACTCT 258
Db 732 CAACTACCCCT 722

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RESULT 8
US-09-328-111-618/c
; Sequence 618, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilison O.
; APPLICANT: Steinhmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 618
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-618

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Query Match      11.3%; Score 30.6; DB 3; Length 305;
Best Local Similarity 56.4%; Pred. No. 0.83;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 3 CGGCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGTTTCCCAATC 62
Db 217 CGCMAAATAACAGCATGTTGTTGAACATCCCCCAGTGGGGCTAGAAATCCCCCATG 158

Qy 63 CTCAACTCTGCTGCGAGCTGATGAGGGAGGAGGGA 103
Db 157 GTGACCTGTGACCTGCTCCCTGAGACAGGGAGGCCAGGCA 117

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RESULT 9
US-09-016-434-1143/c
; Sequence 1143, Application US/09016434

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; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhauer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2885 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1478280
; US-09-016-434-1143

Query Match      11.3%; Score 30.6; DB 4; Length 2885;
Best Local Similarity 56.4%; Pred. No. 2.2;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 3 CGGCAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGTTTCCCAATC 62
Db 2633 CGCMAAATAACAGCATGTTGTTGAACATCCCCCAGTGGGGCTAGAAATCCCCCATG 2574

Qy 63 CTCAACTCTGCTGCGAGCTGATGAGGGAGGAGGGA 103
Db 2573 GTGACCTGTGACCTGCTCCCTGAGACAGGGAGGCCAGGCA 2533

RESULT 10
US-08-856-444-1
; Sequence 1, Application US/08856444
; Patent No. 5959081
; GENERAL INFORMATION:
; APPLICANT: Lecka-Czernik, Beata
; TITLE OF INVENTION: No. 5959081el Zinc Binding LIM Protein S2-6
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; ZIP: 77071
; COMPUTER READABLE FORM:

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APPLICANT: Mundy M.D., Gregory R.
APPLICANT: Gosh-Choudhury Ph.D., Nandini
APPLICANT: Feng Ph.D., Jian Q.

Mon Sep 13 07:48:10 2004

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: James C. Weseman, Esq.
STREET: 401 B. Street, Suite 1700
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,434A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weseman, James C.
REGISTRATION NUMBER: 30,507
REFERENCE/DOCKET NUMBER: P00060USO
TELEPHONE: (619) 699-3604
TELEFAX: 619-236-1048
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9299 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-458-434A-7

Query Match 10.9%; Score 29.6; DB 3; Length 9299;
Best Local Similarity 59.5%; Pred. No. 8.2;
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 150 CGCCCATCCCGACCTTGGCTTACCTACCTCCCAACCTCCCGAGGAGGAGCTATTTA 209
Db 6318 CCCCCACCCCGCCCTTCTCGCCCTCCAGCCCAATTTCACAACTCCAGCTGTGA 6259
QY 210 AGGGAGGAGGAGTGCAGAACAAA 233
Db 6258 AGAAGGAGGAGGGGAGAACAGA 6235

RESULT 14
US-09-014-969-12
Sequence 12, Application US/09014969
Patent No. 5965397

GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaValle, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3111 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-014-969-12

Query Match 10.8%; Score 29.2; DB 2; Length 3111;
Best Local Similarity 57.8%; Pred. No. 6.9;
Matches 52; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 72 GTCCTGCCAGCTGATGAGGGAAGAAAGGATTACCTAGGGGTATGGCGCAATCCT 131
Db 957 GTCGTCCCGGCTGATCAGAGCTTGAGATAGAAAGACTACAGCTGAGCTGTCATCCC 1016
QY 132 GAGTCCCACTGACGCGCCATCCCA 161
Db 1017 CATGCGGATCTTCCACACCCGCTCA 1046

RESULT 15

US-09-506-729-37/c
Sequence 37, Application US/09506729
Patent No. 6365352
GENERAL INFORMATION:
APPLICANT: Yerramilli, Subrahmanyam V.
APPLICANT: Prashar, Yatindra
APPLICANT: Newberger, Peter
APPLICANT: Goguen, Jon
APPLICANT: Weissman, Sherman M.
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
TITLE OF INVENTION: GRANDLOCYTIC CELLS
FILE REFERENCE: 44921-5016-US
CURRENT APPLICATION NUMBER: US/09/506,729
CURRENT FILING DATE: 2000-02-18
EARLIER APPLICATION NUMBER: PCT/US98/17284
EARLIER FILING DATE: 1998-08-21
EARLIER APPLICATION NUMBER: 60/056,844
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 204
TYPE: DNA
ORGANISM: Homo sapiens
US-09-506-729-37

Query Match 10.7%; Score 29; DB 4; Length 204;
Best Local Similarity 57.0%; Pred. No. 2.4;
Matches 53; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 4 GCGAAACTGCCTGAAATGTTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCC 63
Db 194 GGAACATCGCTGCCCAATGAGTGGTGGTGCATGCTTCTTAGGATGCTGATGC 135
QY 64 TCAACTCTGCTGCCAGCTGATGAGGGAAGG 96
Db 134 TGCACGCCAGCTTGAAGCTGCAGAGGGAAGG 102

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Page 7

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Title: US-09-808-388-4

Perfect score: 52

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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
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20: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	52	9	US-09-808-388-4
2	27	51.9	4060	17	US-10-437-963-42345
3	25.2	48.5	42334	12	US-10-052-482-94
4	24.8	47.7	408	15	US-10-214-684A-3
5	24.4	46.9	1350	13	US-10-282-132A-28035
6	23.6	45.4	1821	16	US-10-260-238-1420
7	23.4	45.0	480	13	US-10-027-632-51055
8	23.4	45.0	480	16	US-10-027-632-51055
9	23.4	45.0	517	13	US-10-027-632-51055
10	23.4	45.0	517	16	US-10-027-632-51055
11	23.2	44.6	12596	16	US-10-292-798-889
12	23.2	44.6	12839	15	US-10-017-161-1047
13	23	44.2	559	13	US-10-027-632-245490
14	23	44.2	559	13	US-10-027-632-245491

15	23	44.2	559	16	US-10-027-632-245490	Sequence 245490,
16	23	44.2	559	16	US-10-027-632-245491	Sequence 245491,
17	23	44.2	867	9	US-09-770-445-571	Sequence 571, App
18	23	44.2	3077	15	US-10-128-714-349	Sequence 349, App
19	23	44.2	3078	15	US-10-128-714-5349	Sequence 5349, App
20	23	44.2	26047	13	US-10-087-192-598	Sequence 598, App
21	23	44.2	247461	17	US-10-322-281-131	Sequence 131, App
22	22.8	43.8	60	10	US-09-877-705A-142	Sequence 142, App
23	22.8	43.8	60	10	US-09-877-738A-142	Sequence 142, App
24	22.8	43.8	60	13	US-09-947-274-142	Sequence 142, App
25	22.8	43.8	60	17	US-10-779-595-142	Sequence 142, App
26	22.8	43.8	559	13	US-10-027-632-271817	Sequence 271817,
27	22.8	43.8	559	16	US-10-027-632-271817	Sequence 271817,
28	22.8	43.8	632	13	US-10-027-632-271818	Sequence 271818,
29	22.8	43.8	632	16	US-10-027-632-271818	Sequence 271818,
30	22.8	43.8	659	13	US-10-027-632-11556	Sequence 11556, A
31	22.8	43.8	659	16	US-10-027-632-11556	Sequence 11556, A
32	22.8	43.8	1248	13	US-10-027-632-124870	Sequence 124870,
33	22.8	43.8	1248	16	US-10-027-632-124870	Sequence 124870,
34	22.8	43.8	1418	10	US-09-814-353-21334	Sequence 21334, A
35	22.8	43.8	1461	13	US-10-282-122A-22438	Sequence 22438, A
36	22.6	43.5	331	17	US-10-437-963-84032	Sequence 84032, A
37	22.6	43.5	1035	13	US-10-282-122A-15887	Sequence 15887, A
38	22.4	43.1	472	13	US-10-424-599-49385	Sequence 49385, A
39	22.4	43.1	971	13	US-10-425-114-11342	Sequence 11342, A
40	22.4	43.1	994	13	US-10-424-599-3951	Sequence 3951, App
41	22.4	43.1	4290	13	US-10-282-122A-16164	Sequence 16164, App
42	22.2	42.7	451	10	US-09-918-995-2661	Sequence 2661, App
43	22.2	42.7	456	10	US-09-918-995-15681	Sequence 15681, A
44	22.2	42.7	666	13	US-10-027-632-141504	Sequence 141504,
45	22.2	42.7	666	16	US-10-027-632-141504	Sequence 141504,

ALIGNMENTS

RESULT 1
US-09-808-388-4
; Sequence 4, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPPE element
US-09-808-388-4

Query Match 100.0%; Score 52; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCATGCTTTAGGCCCAAACTAGTCAAGGTCA 52
DB 1 CAAACTAGGTCAAAGGTCATGCTTTAGGCCCAAACTAGTCAAGGTCA 52

RESULT 4
US-10-214-684A-3
; Sequence 3, Application US/10214684A
; Publication No. US20030190636A1

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; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 1420
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Oriza sativa
US-10-260-238-1420

Query Match      45.4%; Score 23.6; DB 16; Length 1821;
Best Local Similarity 69.6%; Pred. No. 43;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 2 AAACTAGGTCAAAGGTCATGCTTTAGGCCAAAACCTAGGTCAA 47
DB 1645 AAAGCCAAAGTAACAGTTGACATCCATAGTCCCAACACTAGACAAA 1600

RESULT 7
US-10-027-632-51055/c
; Sequence 51055, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 51055
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51055

Query Match      45.0%; Score 23.4; DB 13; Length 480;
Best Local Similarity 81.8%; Pred. No. 36;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCATGCTTTAGGCC 33
DB 137 CACACCTTGGCTAGATAAATGCTTTAGGCC 105

RESULT 8
US-10-027-632-51055/c
; Sequence 51055, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12

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; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51055
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51055

Query Match          45.0%; Score 23.4; DB 16; Length 480;
Best Local Similarity 81.8%; Pred. No. 36;
Matches      27; Conservative    0; Mismatches     6; Indels   0; Gaps   0;

QY      1 CAAAACTAGGTCAAAGGTCAATGCTTTTAGGCC 33
Db      137 CACACCTTGGTGCTAAGATAATGCTTTTAGGCC 105

RESULT 9
US-10-027-632-82715
; Sequence 82715, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82715
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-82715

Query Match          45.0%; Score 23.4; DB 13; Length 517;
Best Local Similarity 81.8%; Pred. No. 37;
Matches      27; Conservative    0; Mismatches     6; Indels   0; Gaps   0;

QY      1 CAAAACTAGGTCAAAGGTCAATGCTTTTAGGCC 33
Db      330 CACACCTTGGTGCTAAGATAATGCTTTTAGGCC 362

RESULT 10
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6614)..(6713)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11526)..(12396)
US-10-292-798-889

Query Match
Best Local Similarity 44.6%; Score 23.2; DB 16; Length 12596;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 8 AGGTCAAGGTCATGCTTTTAGGCCCAAACTAGGT 43
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Db 8424 AGGTAAAGGTCAGGCTATCAGGCCCAAACTGGGT 8459

RESULT 12
US-10-017-161-1047
; Sequence 1047, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1047
; LENGTH: 12839
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(12839)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(240)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (962)..(1276)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6743)..(6842)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11556)..(12639)
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (3251)..(3350)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified base
; LOCATION: (12171)..(12270)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-1047

Query Match
Best Local Similarity 44.6%; Score 23.2; DB 15; Length 12839;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 8 AGGTCAAGGTCATGCTTTTAGGCCCAAACTAGGT 43
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Db 8553 AGGTAAAGGTCAGGCTATCAGGCCCAAACTGGGT 8588

RESULT 13
US-10-027-632-245490
; Sequence 245490, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245490
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-245490

Query Match
Best Local Similarity 44.2%; Score 23; DB 13; Length 559;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 AAAGTGGTCAAGGTCATGCTTTTAGGCCCAAACTAGGTCAAAGG 49
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Db 167 AAGCATAGAAAAAAGGTCATGCTGAAGGCTCAAAGTAGGAAAGG 213

RESULT 14
US-10-027-632-245491
; Sequence 245491, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245491
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-245491
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Job time : 51.4382 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 08:16:17 ; Search time 8.17668 Seconds
(without alignments)
3529.238 Million cell updates/sec

Title: US-09-808-388-4

Perfect score: 52

Sequence: 1 caaaactagggtcaaggtca.....caaaactagggtcaaggtca 52

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents NA:*

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24.8	47.7	408	4	US-09-499-522-3
2	23.2	44.6	232	5	PCT-US93-06251-44
3	21.8	41.9	900	4	US-09-134-000C-1316
4	21.8	41.9	72928	3	US-09-009-913-1
5	21.4	41.2	352	4	US-09-023-655-361
6	21.2	40.8	2073	4	US-09-489-039A-6817
7	21.2	40.8	3135	4	US-08-956-171B-461
8	20.8	40.0	498	4	US-09-328-475C-218
9	20.8	40.0	541	4	US-09-404-879A-26
10	20.8	40.0	541	4	US-09-338-933-26
11	20.8	40.0	541	4	US-09-215-681-26
12	20.8	40.0	541	4	US-09-216-003A-26
13	20.8	40.0	1312	4	US-09-328-475C-335
14	20.8	40.0	3970	1	US-07-925-695-3
15	20.8	40.0	5531	4	US-09-620-312D-619
16	20.8	40.0	9589	1	US-07-925-695-1
17	20.8	40.0	9589	1	US-07-925-695-2
18	20.6	39.6	1298	4	US-09-311-784A-25
19	20.6	39.6	2072	4	US-09-725-735A-11
20	20.6	39.6	2455	1	US-08-073-807A-1
21	20.6	39.6	2829	4	US-09-489-039A-6811
22	20.6	39.6	4052	1	US-08-057-167-1
23	20.6	39.6	4052	5	PCT-US93-05412-1
24	20.6	39.6	5046	4	US-09-725-735A-13
25	20.6	39.6	246240	2	US-08-724-394A-20
26	20.6	39.6	246240	2	US-08-724-394A-21
27	20.6	39.6	246240	2	US-08-724-394A-22

28 20.4 39.2 3022 4 US-09-232-278A-8
29 20.4 39.2 3177 3 US-09-058-489-50
30 20.4 39.2 3674 1 US-08-105-483-324
31 20.4 39.2 3674 1 US-08-709-209-324
32 20.4 39.2 3674 1 US-08-458-101-324
33 20.4 39.2 269223 4 US-09-596-002-41
34 20.2 38.8 328 1 US-08-455-550-5
35 20.2 38.8 1001 4 US-09-671-317-4
36 20.2 38.8 1201 4 US-09-205-448-3
37 20.2 38.8 2385 4 US-09-134-000C-2113
38 20.2 38.8 2931 4 US-09-623-624-1
39 20.2 38.8 49312 4 US-09-671-317-485
40 20.2 38.5 161652 4 US-09-497-855A-40
41 20 38.5 451 4 US-09-621-976-1739
42 20 38.5 1365 4 US-09-540-236-331
43 20 38.5 1434 4 US-09-328-352-3639
44 20 38.5 4808 1 US-08-351-413-17
45 20 38.5 4808 2 US-09-025-583-17

ALIGNMENTS

RESULT 1
US-09-499-522-3
; Sequence 3, Application US/09499522
; Patent NO. 6479238
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: POLYMORPHIC MARKERS OF THE LSR GENE
; FILE REFERENCE: GENSET.053AUS
; CURRENT APPLICATION NUMBER: US/09/499,522
; CURRENT FILING DATE: 2000-02-10
; EARLIER APPLICATION NUMBER: US 60/119,592
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: US 60/144,784
; EARLIER FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent.pm
; SEQ ID NO 3
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 353
; OTHER INFORMATION: 99-14424-353 : polymorphic base A or G
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 334..352
; OTHER INFORMATION: 99-14424-353.misl real
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 354..376
; OTHER INFORMATION: 99-14424-353.mis2 potential, complement
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 388..408
; OTHER INFORMATION: downstream amplification primer, complement
US-09-499-522-3

Query Match 47.7%; Score 24.8; DB 4; Length 408;
Best Local Similarity 80.6%; Pred. No. 0.49;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 12 CAAAGGTATGTCTTAGCGCCAAACAGTGTCAA 47

|||||

Db

348 CACACGACATGGCTTTAGGCCCCCAACAAGGTAAAA 383

RESULT 2

PCT-US93-06251-44/c

; Sequence 44, Application PC/TUS9306251

; GENERAL INFORMATION:

; APPLICANT: Wickstrom, Eric and Rife, Jason P.

; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing

; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates

; NUMBER OF SEQUENCES: 93

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: NY

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/06251

; FILING DATE: 19930630

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Digiglio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8586

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 516-742-4343

; TELEFAX: 516-742-4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 44:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 232 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

PCT-US93-06251-44

Query Match 44.6%; Score 23.2; DB 5; Length 232;

Best Local Similarity 70.5%; Pred. No. 1.9;

Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 AAAACTAGTCAAGGTCATGCTTTAGGCCCAAACTAGGTCA 45

Db 73 AAAAGTAGTCTTTGGTCGGGTTCTTAGGCCCAAGCACTGGGTCA 30

RESULT 3

US-09-134-000C-1316/c

; Sequence 1316, Application US/09134000C

; Patent No. 6617156

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 032796-032

; CURRENT APPLICATION NUMBER: US/09/134,000C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/055,778

; PRIOR FILING DATE: 1997-08-15

; NUMBER OF SEQ ID NOS: 6812

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1316

; LENGTH: 900

; TYPE: DNA

; ORGANISM: Enterococcus faecalis

US-09-134-000C-1316

Query Match 41.9%; Score 21.8; DB 3; Length 72928;

Best Local Similarity 65.3%; Pred. No. 32;

Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2 AAAACTAGTCAAGGTCATGCTTTAGGCCCAAACTAGGTCA 50

Db 37573 AAAAGTTGATCAATGTCATCTCTTTCTCACGAATCTTGGTCATGTGT 37621

RESULT 5

US-09-023-655-361

; Sequence 361, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

US-09-023-655-361

Query Match 41.9%; Score 21.8; DB 3; Length 72928;

Best Local Similarity 65.3%; Pred. No. 32;

Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2 AAAACTAGTCAAGGTCATGCTTTAGGCCCAAACTAGGTCA 50

Db 37573 AAAAGTTGATCAATGTCATCTCTTTCTCACGAATCTTGGTCATGTGT 37621

RESULT 4

US-09-009-913-1

; Sequence 1, Application US/09009913

; Patent No. 6087485

; GENERAL INFORMATION:

; APPLICANT: Axys Pharmaceuticals, Inc.

; TITLE OF INVENTION: Asthma Related Genes

; NUMBER OF SEQUENCES: 339

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bozicevic & Reed, LLP

; STREET: 285 Hamilton Ave, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,913

; FILING DATE: 21-JAN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sherwood, Pamela J

; REGISTRATION NUMBER: 36,677

; REFERENCE/DOCKET NUMBER: SEQ-4P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-327-3231

; TELEFAX: 650-327-3231

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 72928 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA

US-09-009-913-1

Query Match 41.9%; Score 21.8; DB 3; Length 72928;

Best Local Similarity 65.3%; Pred. No. 32;

Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2 AAAACTAGTCAAGGTCATGCTTTAGGCCCAAACTAGGTCA 50

Db 37573 AAAAGTTGATCAATGTCATCTCTTTCTCACGAATCTTGGTCATGTGT 37621


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; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 218
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-328-475C-218

Query Match      40.0%; Score 20.8; DB 4; Length 498;
Best Local Similarity 64.6%; Pred. No. 22;
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY      2 AAACCTAGTCAAAGTCAATGCTCTTTAGGCCCAAACTAGGTCAAAGG 49
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DB      152 AAACCTAGTGTGAGTGACTGTGTCACAGTTCCTCAAGCTTAATAAATG 199

RESULT 9
US-09-404-879A-26/c
; Sequence 26, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-26

Query Match      40.0%; Score 20.8; DB 4; Length 541;
Best Local Similarity 78.1%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      6 CTAGGTCAAAGTCAATGCTCTTTAGGCCCAAAA 37
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      294 CAAGTCAAGGACATGCTTTTAGCCCCCAA 263

RESULT 10
US-09-338-933-26/c
; Sequence 26, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-338-933-26

Query Match      40.0%; Score 20.8; DB 4; Length 541;
Best Local Similarity 78.1%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      6 CTAGGTCAAAGTCAATGCTCTTTAGGCCCAAAA 37
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      294 CAAGTCAAGGACATGCTTTTAGCCCCCAA 263

RESULT 11
US-09-215-681-26/c
; Sequence 26, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF OVARIAN CANCER
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-215-681-26

Query Match      40.0%; Score 20.8; DB 4; Length 541;
Best Local Similarity 78.1%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      6 CTAGGTCAAAGTCAATGCTCTTTAGGCCCAAAA 37
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      294 CAAGTCAAGGACATGCTTTTAGCCCCCAA 263

RESULT 12
US-09-216-003A-26/c
; Sequence 26, Application US/09216003A
; Patent No. 6670463
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
; FILE REFERENCE: 210121.462
; CURRENT APPLICATION NUMBER: US/09/216,003A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-216-003A-26

Query Match      40.0%; Score 20.8; DB 4; Length 541;
Best Local Similarity 78.1%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      6 CTAGGTCAAAGTCAATGCTCTTTAGGCCCAAAA 37
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      294 CAAGTCAAGGACATGCTTTTAGCCCCCAA 263

RESULT 13
US-09-328-475C-335/c
; Sequence 335, Application US/09328475C
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 09:20:47 ; Search time 39.7686 Seconds
(without alignments)
5187.326 Million cell updates/sec

Title: US-09-808-388-3

Perfect score: 41

Sequence: 1 caaaactagggtcaaaagggtca.....caaaactagggtcaaaagggtca 41

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*

17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*

18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	41	9	US-09-808-388-3
2	41	100.0	332	9	US-09-808-388-6
3	29	70.7	60	10	US-09-877-705A-142
4	29	70.7	60	10	US-09-877-738A-142
5	29	70.7	60	13	US-09-947-274-142
6	29	70.7	60	17	US-10-779-595-142
7	25	61.0	38	9	US-09-808-388-2
8	24.6	60.0	85859	13	US-10-087-192-562
9	23.6	57.6	177556	10	US-09-952-213D-6
10	23.2	56.6	582	13	US-10-424-599-53103
11	23	56.1	580073	15	US-10-205-220-1
12	22.4	54.6	862	13	US-10-424-599-139279
13	22.4	54.6	3295	10	US-09-952-267-8
14	22.4	54.6	3349	10	US-09-952-267-2

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15      22.2      54.1      3130      13      US-10-424-599-56034
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c 17      22      53.7      2940917      16      US-10-027-632-174763
c 18      21.6      52.7      785      13      US-10-027-632-158189
c 19      21.6      52.7      785      13      US-10-027-632-158189
c 20      21.6      52.7      785      16      US-10-027-632-158189
c 21      21.6      52.7      785      16      US-10-027-632-158189
c 22      21.6      52.7      715517      13      US-10-027-632-53712
c 23      21.6      52.7      715517      16      US-10-027-632-53712
c 24      21.4      52.2      430      15      US-10-102-524-1082
c 25      21.4      52.2      474      10      US-09-918-995-29668
c 26      21.4      52.2      512      15      US-10-102-524-433
c 27      21.4      52.2      634      15      US-10-060-036-215
c 28      21.4      52.2      851      17      US-10-437-963-50885
c 29      21.4      52.2      910      15      US-10-190-312A-86
c 30      21.4      52.2      978      13      US-10-027-632-324444
c 31      21.4      52.2      978      16      US-10-027-632-324444
c 32      21.4      52.2      2595      15      US-10-106-698-451
c 33      21.4      52.2      2930      17      US-09-960-253-156
c 34      21.4      52.2      2930      17      US-10-450-826-88
c 35      21.4      52.2      3044      9      US-09-880-107-3718
c 36      21.4      52.2      3044      17      US-10-450-826-87
c 37      21.4      52.2      3044      17      US-10-776-827-84
c 38      21.4      52.2      3047      9      US-09-864-864-329
c 39      21.4      52.2      3064      15      US-10-007-926A-53
c 40      21.4      52.2      3072      17      US-10-450-826-89
c 41      21.4      52.2      3115      9      US-09-925-299-123
c 42      21.4      52.2      3115      10      US-09-925-299-123
c 43      21.4      52.2      3166      16      US-10-159-563-357
c 44      21.4      52.2      5253      13      US-10-424-599-131924
c 45      21.4      52.2      26345      13      US-10-087-192-1705

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ALIGNMENTS

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RESULT 1
US-09-808-388-3
; Sequence 3, Application US/09/808,388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE element
US-09-808-388-3

Query Match      100.0%; Score 41; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      CAAAACCTAGGTCAAAAGGTCAATCAAACTAGGTCAAAAGGTCA 41
Db      1      CAAAACCTAGGTCAAAAGGTCAATCAAACTAGGTCAAAAGGTCA 41

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Mon Sep 13 07:48:09 2004

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; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-877-738A-142

Query Match 70.7%; Score 29; DB 10; Length 60;
Best Local Similarity 97.6%; Pred. No. 0.19;
Matches 40; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAAACTAGGTCAAAGGTCATCAAACTAGGTCAAAGGTCA 41
| | | | | | | | | | | | | | | | | | | | | |
DB 60 CAAAACTAGGTCAAAGGTCATCAAACTAGGTCAAAGGTCA 21

RESULT 5
US-09-947-274-142/c
; Sequence 142, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947,274
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877,738
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,243
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,403
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,705
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-947-274-142

Query Match 70.7%; Score 29; DB 13; Length 60;
Best Local Similarity 97.6%; Pred. No. 0.19;
Matches 40; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAAACTAGGTCAAAGGTCATCAAACTAGGTCAAAGGTCA 41
| | | | | | | | | | | | | | | | | | | | | |
DB 60 CAAAACTAGGTCAAAGGTCATCAAACTAGGTCAAAGGTCA 21

RESULT 6
US-10-779-595-142/c
; Sequence 142, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACT
; FILE REFERENCE: 26757-702.301
; CURRENT APPLICATION NUMBER: US/10/779,595
; CURRENT FILING DATE: 2004-02-13

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; PRIOR APPLICATION NUMBER: 09/877,243
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-10-779-595-142

Query Match 70.7%; Score 29; DB 17; Length 60;
Best Local Similarity 97.6%; Pred. No. 0.19;
Matches 40; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CAAACTAGTCAAGGTCATCAAACTAGGTCAAAGGTCA 41
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Db 60 CAAACTAGTCAAGGTCATCAAACTAGGTCAAAGGTCA 21
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RESULT 7

US-09-808-388-2
; Sequence 2, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Bereziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PPRE element
US-09-808-388-2

Query Match 61.0%; Score 25; DB 9; Length 38;
Best Local Similarity 92.7%; Pred. No. 5.5;
Matches 38; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 CAAACTAGTCAAGGTCATCAAACTAGGTCAAAGGTCA 41
|||||
Db 1 CAAACTAGTCAAGG---TCAAACTAGGTCAAAGGTCA 38
|||||

RESULT 8

US-10-087-192-562/c
; Sequence 562, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 562
; LENGTH: 85859
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..- (85859)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-562

Query Match 60.0%; Score 24.6; DB 13; Length 85859;
Best Local Similarity 76.9%; Pred. No. 56;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 AAACCTAGGTCAAGGTCATCAAACTAGGTCAAAGGTCA 41
|||||
Db 9276 AAACATCTCAAGGACATAAACACTATGTCAAGGACA 9238
|||||

RESULT 9

US-09-952-213D-6/c
; Sequence 6, Application US/09952213D
; Publication No. US20030096240A1
; GENERAL INFORMATION:
; APPLICANT: MURAD, FERID
; APPLICANT: SHARINA, IRAIDA G.
; APPLICANT: KRUMENACKER, J. S.
; APPLICANT: MARTIN, E.
; TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE AND HUMAN SCG
; FILE REFERENCE: UTSH:252US
; CURRENT APPLICATION NUMBER: US/09/952,213D
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 177556
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (2293..144567)
; OTHER INFORMATION: N = A, C, T/U OR G
US-09-952-213D-6

Query Match 57.6%; Score 23.6; DB 10; Length 177556;
Best Local Similarity 76.3%; Pred. No. 1.6e+02;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 AAACCTAGGTCAAGGTCATCAAACTAGGTCAAAGGT 39
|||||
Db 120237 AAATCCAGGTGAGGTCATGAAGGCTGGGCAAGGT 120200
|||||

RESULT 10

US-10-424-599-53103/c
; Sequence 53103, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 53103

Query Match 54.6%; Score 22.4; DB 13; Length 862;
Best Local Similarity 72.5%; Pred. No. 1.2e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2 AAAAAGTGGTCAAAAGGTCATCAAAAGTGGTCAAAAGGTC 41
DB 631 AAGATGATGACAAAGGTCATGACAAAGGTC 592
RESULT 13
US-09-952-267-8
; Sequence 8, Application US/09952267
; Publication No. US20030032772A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/952,267
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3295
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-09-952-267-8
Query Match 54.6%; Score 22.4; DB 10; Length 3295;
Best Local Similarity 72.5%; Pred. No. 1.6e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 CAAAAGTGGTCAAAAGGTCATCAAAAGTGGTCAAAAGGTC 40
DB 2118 CAAGATATATCAAAAGATCTTCAGAGGAGGTCAGAGGTC 2157
RESULT 14
US-09-952-267-2
; Sequence 2, Application US/09952267
; Publication No. US20030032772A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/952,267
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3349
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-09-952-267-2
Query Match 54.6%; Score 22.4; DB 10; Length 3349;
Best Local Similarity 72.5%; Pred. No. 1.7e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 CAAAAGTGGTCAAAAGGTCATCAAAAGTGGTCAAAAGGTC 40

US-10-424-599-53103
Query Match 56.6%; Score 23.2; DB 13; Length 582;
Best Local Similarity 77.8%; Pred. No. 53;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 CAAAAGTGGTCAAAAGGTCATCAAAAGTGGTCAAA 36
DB 527 CAAAGTGGTCAAAAGGTAACCATTAAGTGGTATA 492
RESULT 11
US-10-205-220-1/c
; Sequence 1, Application US/10205220
; Publication No. US20030170663A1
; GENERAL INFORMATION:
; APPLICANT: Fraser et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
; FILE REFERENCE: PB193P1D1
; CURRENT APPLICATION NUMBER: US/10/205,220
; CURRENT FILING DATE: 2002-07-26
; PRIOR FILING DATE: 1995-10-19
; PRIOR APPLICATION NUMBER: US 08/545,528
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/488,018
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/473,545
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 580073
; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-10-205-220-1
Query Match 56.1%; Score 23; DB 15; Length 580073;
Best Local Similarity 74.4%; Pred. No. 3.6e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 3 AAAGTGGTCAAAAGGTCATCAAAAGTGGTCAAAAGGTC 41
DB 21505 AAATTTGGTAAACAAATCAAAAGATCAAGATCA 21467
RESULT 12
US-10-424-599-139279/c
; Sequence 139279, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 139279
; LENGTH: 862
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_96777C.1
US-10-424-599-139279

Db 1311 CAAGATGATATCAAGATCTTCAGAAAGGAGGTGAAAGGTC 1350

RESULT 15

US-10-424-599-56034
; Sequence 56034, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 56034
; LENGTH: 3130
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(3130)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2160C.1
US-10-424-599-56034

Query Match 54.1%; Score 22.2; DB 13; Length 3130;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 AAGGTCATCAAAACTAGGTCAAAGGT 39
Db 1451 AAGGTCATCAAAACTGGTCAAAGTT 1477

Search completed: September 11, 2004, 14:11:15
Job time : 45.7686 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 08:16:17 ; Search time 6.447 Seconds
(without alignments)
3529.238 Million cell updates/sec

Title: US-09-808-388-3
Perfect score: 41
Sequence: 1 caaaactaggtcaaaagggtca.....caaaactaggtcaaaagggtca 41

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	23	56.1	580073	4	US-08-545-528D-1
C 2	22.4	54.6	3295	4	US-09-336-447A-8
C 3	22.4	54.6	3349	4	US-09-336-447A-2
C 4	21.2	51.7	1305	4	US-09-328-352-3178
C 5	21	51.2	865	3	US-09-328-111-128
C 6	20.4	49.8	910	3	US-09-328-111-129
C 7	20.4	49.8	3900	1	US-08-123-343A-6
C 8	20.2	49.3	1140	4	US-09-328-352-1678
C 9	20.2	49.3	2308	1	US-07-686-591-3
C 10	20.2	49.3	2308	1	US-07-970-715-3
C 11	20	48.8	966	4	US-09-328-352-1604
C 12	20	48.8	1200	4	US-09-222-938A-47
C 13	19.8	48.3	1797	2	US-08-366-490-5
C 14	19.8	48.3	1797	3	US-08-860-483A-5
C 15	19.8	48.3	1900	2	US-08-366-490-7
C 16	19.8	48.3	1900	3	US-08-860-483A-8
C 17	19.8	48.3	1900	3	US-08-860-483A-9
C 18	19.8	48.3	3172	4	US-09-976-594-400
C 19	19.8	48.3	15894	1	US-08-348-891A-1
C 20	19.8	48.3	15894	1	US-08-905-817-1
C 21	19.8	48.3	19056	3	US-09-272-032-8
C 22	19.8	48.3	19056	4	US-09-443-218-8
C 23	19.6	47.8	2868	2	US-08-389-564B-3
C 24	19.6	47.8	2868	3	US-08-466-047B-3
C 25	19.4	47.3	384	4	US-09-107-532A-1817
C 26	19.4	47.3	1143	4	US-09-170-496D-61
C 27	19.4	47.3	1143	4	US-09-170-496D-197

C 28 19.4 47.3 1317 4 US-09-328-352-2385 Sequence 2385, Ap
C 29 19.4 47.3 1464 4 US-09-149-045-1 Sequence 1, Appli
C 30 19.4 47.3 1583 4 US-09-016-434-1365 Sequence 1365, Ap
C 31 19.4 47.3 1749 4 US-09-081-149-6 Sequence 6, Appli
C 32 19.4 47.3 1758 4 US-09-255-518C-4 Sequence 4, Appli
C 33 19.4 47.3 1834 4 US-09-843-472-5 Sequence 5, Appli
C 34 19.4 47.3 1872 1 US-08-153-848-39 Sequence 39, Appl
C 35 19.4 47.3 1872 3 US-09-299-843A-39 Sequence 39, Appl
C 36 19.4 47.3 1872 4 US-09-088-337B-39 Sequence 70, Appl
C 37 19.4 47.3 1872 5 PCT-US93-11153-39 Sequence 21, Appl
C 38 19.4 47.3 2462 4 US-09-220-132-70 Sequence 22, Appl
C 39 19.4 47.3 10432 4 US-09-919-172-97 Sequence 97, Appl
C 40 19.4 47.3 10432 4 US-09-976-594-21 Sequence 21, Appl
C 41 19.2 46.8 132 1 US-08-053-171-23 Sequence 23, Appl
C 42 19.2 46.8 849 4 US-09-540-236-656 Sequence 656, App
C 43 19.2 46.8 1001 4 US-09-641-638-480 Sequence 480, App
C 44 19.2 46.8 1001 4 US-09-641-638-481 Sequence 481, App
C 45 19.2 46.8 1001 4 US-09-641-638-482 Sequence 482, App

ALIGNMENTS

RESULT 1

US-08-545-528D-1/c
; Sequence 1, Application US/08545528D
; Patent No. 6537773

; GENERAL INFORMATION:

; APPLICANT: Fraser et al.

; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment;
; Patent No. 6537773

; FILE REFERENCE: PB193P1

; CURRENT APPLICATION NUMBER: US/08/545,528D

; CURRENT FILING DATE: 1995-10-19

; PRIOR APPLICATION NUMBER: US 08/488,018

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: US 08/473,545

; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 580073

; TYPE: DNA

; ORGANISM: Mycoplasma genitalium

US-08-545-528D-1

Query Match 56.1%; Score 23; DB 4; Length 580073;
Best Local Similarity 74.4%; Pred. No. 14;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3 AAACAGGTCAAGGTCAATCAAAAGTGGTCAAGGTCA 41

Db 21505 AAATTGGTAAACAAATCAAAACAGATCA 21467

RESULT 2

US-09-336-447A-8

; Sequence 8, Application US/09336447A

; Patent No. 6310190

; GENERAL INFORMATION:

; APPLICANT: HANSEN, ERIC J.

; APPLICANT: ABEI, CHRISTOPH

; APPLICANT: COPE, LESLIE D.

; APPLICANT: MACIVER, ISOBEL

; APPLICANT: FISKE, MICHAEL J.

; APPLICANT: FREDENBURG, ROSS A.

; TITLE OF INVENTION: USP41 AND USP42 ANTIGENS OF MORAXELLA CATARRHALIS

; FILE REFERENCE: AMCY:024

; CURRENT APPLICATION NUMBER: US/09/336,447A

; CURRENT FILING DATE: 1999-06-21

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 8
; LENGTH: 3295
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-8

Query Match          54.6%; Score 22.4; DB 4; Length 3295;
Best Local Similarity 72.5%; Pred. No. 6.4; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 11;

QY      1 CAAAACCTAGGTCAAAGGTCATCAAAACTAGGTCAAAGGC 40
       ||| | | | | | | | | | | | | | | | | | | | | |
DB     2118 CAAGAATAATCAAGATCTTCAAGAGGAGGTGAAGGC 2157


RESULT 3
US-09-336-447A-2
; Sequence 2, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPAl AND USP2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3349
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-2

Query Match          54.6%; Score 22.4; DB 4; Length 3349;
Best Local Similarity 72.5%; Pred. No. 6.5; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 11;

QY      1 CAAAACCTAGGTCAAAGGTCATCAAAACTAGGTCAAAGGC 40
       ||| | | | | | | | | | | | | | | | | | | | | |
DB     1311 CAAGATGATACAAGATCTTCAGAAGGAGGTCAAAGGC 1350


RESULT 4
US-09-328-352-3178/c
; Sequence 3178, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3178
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3178

Query Match          51.7%; Score 21.2; DB 4; Length 1305;
Best Local Similarity 76.5%; Pred. No. 15; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 8;

QY      2 AAAACCTAGGTCAAAGGTCATCAAAACTAGGTCAA 35
       ||| | | | | | | | | | | | | | | | | | | | | |
DB     65 ATAAAGAGGGCAAGGTCATAAACCCTAAGGCAA 32

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RESULT 5
US-09-328-111-128/c
; Sequence 128, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 128
; LENGTH: 865
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(865)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-128

Query Match          51.2%; Score 21; DB 3; Length 865;
Best Local Similarity 71.1%; Pred.No.16;
Matches 27; Conservative 0; Mismatches 11; Indels

QY 1 CAAAAGTAGGTCAAAGTCATCAAAAGTAAAGTAAAGTCAAAGG 38
DB 595 CAAAATAGNCAAAGGCGCAAGGAACCTTTGCCAAAGG 558

RESULT 6
US-09-328-111-129
; Sequence 129, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 129

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Query Match	49.8%;	Score 20.4;	DB 1;	Length 3900;
Best Local Similarity	71.1%;	Pred. No. 42;		
Matches 27;	Conservative 0;	Mismatches 11;	Indels 0;	Gaps 0;
QY	2	AAACTAGTGTCAAAGGTCATCAAAACTAGGTCAAAGGT	39	
DB	2126	AAATGCAATCAAGATTATCAAAAGTATCTCAAAAGT	2089	

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1  RESULT 9
2  US-07-686-591-3
3  ; Sequence 3, Application US/07686591
4  ; Patent No. 5215915
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Tiberi, Mario
7  ; APPLICANT: Jarvie, Keith R.
8  ; APPLICANT: Caron, Marc G.
9  ; TITLE OF INVENTION: Cloned Gene Encoding Rat D1B Dopamine Receptor
10 ; NUMBER OF SEQUENCES: 4
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and Gibson
13 ; STREET: Post Office Drawer 34009
14 ; CITY: Charlotte
15 ; STATE: No. 5215915th Carolina
16 ; COUNTRY: U.S.A.
17 ; ZIP: 28234
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.24
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/07/686,591
25 ; FILING DATE: 19910406
26 ; CLASSIFICATION: 435
27 ; ATTORNEY/AGENT INFORMATION:
28 ; NAME: Sibley, Kenneth D.
29 ; REGISTRATION NUMBER: 31,665
30 ; REFERENCE/DOCKET NUMBER: 5405.24
31 ; TELECOMMUNICATION INFORMATION:
32 ; TELEPHONE: 919-881-3140
33 ; TELEFAX: 919-881-3175
34 ; TELEX: 575102
35 ; INFORMATION FOR SEQ ID NO: 3:
36 ; SEQUENCE CHARACTERISTICS:
37 ; LENGTH: 2308 base pairs
38 ; TYPE: NUCLEIC ACID
39 ; STRANDEDNESS: single
40 ; TOPOLOGY: linear
41 ; MOLECULE TYPE: DNA (genomic)
42 ; HYPOTHETICAL: N
43 ; ANTI-SENSE: N
44 ; FEATURE:
45 ; NAME/KEY: CDS

```

; NUMBER OF SEQUENCES: 10

/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
/ STREET: 277 Park Avenue
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10172-0194
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/366,490
/ FILING DATE: 30-DEC-1994
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitzpatrick, Cella, Harper, and Scinto
/ REFERENCE/DOCKET NUMBER: 4869
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-758-2400
/ TELEFAX: 212-758-2982
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1797 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ ORIGINAL SOURCE:
/ ORGANISM: PAPAYA RINGSPOT VIRUS
/ STRAIN: P-TYPE
/ INDIVIDUAL ISOLATE: USA (HA attenuated)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 3..1782
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 3..191
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 192..362
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 363..1643
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 1644..1782
/ US-08-366-490-5

Query Match 48.3%; Score 19.8; DB 2; Length 1797;
Best Local Similarity 69.2%; Pred.No. 60;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CAAAGCTAGGTCAGGTCATCAAACTAGGTCAAAGGT 39
Db 1214 CAGAGCTAGGTTTAGGGCCATGAAGCTGGGACAGGT 1252

RESULT 14
US-08-483A-5
; Sequence 5, Application US/08860483A
; Patent No. 6048384
; GENERAL INFORMATION:
; APPLICANT: McMaster, J. R.
; APPLICANT: Boeshore, Maury L.
; APPLICANT: Tricoli, David M.
; APPLICANT: Reynolds, John F.
; APPLICANT: Carney, Kim J.
; APPLICANT: Slignton, Jerry L.

/ APPLICANT: Gonsalves, Dennis
/ TITLE OF INVENTION: Papaya Ringspot Virus Nia Protease Gene
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Rockey, Milnamow & Katz
/ STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
/ CITY: Suite 4700
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/860,483A
/ FILING DATE: 26-JUN-1997
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mueller, Lisa V.
/ REGISTRATION NUMBER: 38,978
/ REFERENCE/DOCKET NUMBER: SVS3801P0091US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 3126165400
/ TELEFAX: 3126165460
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1797 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 3..1779
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1782..1797
/ US-08-860-483A-5

Query Match 48.3%; Score 19.8; DB 3; Length 1797;
Best Local Similarity 69.2%; Pred.No. 60;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CAAAGCTAGGTCAGGTCATCAAACTAGGTCAAAGGT 39
Db 1214 CAGAGCTAGGTTTAGGGCCATGAAGCTGGGACAGGT 1252

RESULT 15
US-08-366-490-7
; Sequence 7, Application US/08366490
; Patent No. 5877403
; GENERAL INFORMATION:
; APPLICANT: McMaster, J. Russell
; APPLICANT: Boeshore, Maury L.
; APPLICANT: Tricoli, David M.
; APPLICANT: Reynolds, John F.
; APPLICANT: Carney, Kim J.
/ TITLE OF INVENTION: PAPAYA RINGSPOT VIRUS PROTEASE GENE
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10172-0194
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible

Mon Sep 13 07:48:09 2004

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,490
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Fitzpatrick, Cella, Harper, and Scinto
REFERENCE/DOCKET NUMBER: 4869
TELEPHONE: 212-758-2400
TELEFAX: 212-758-2982
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: PAPAYA RINGSPOT VIRUS
STRAIN: P-TYPE
INDIVIDUAL ISOLATE: Hawaii
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1900
PUBLICATION INFORMATION:
AUTHORS: Yeh, SD
AUTHORS: Jan, F
AUTHORS: Chiang, C
AUTHORS: Doong, T
AUTHORS: Chen, M
AUTHORS: Chung, P
AUTHORS: Bau, H
TITLE: Complete nucleotide sequence and genetic
TITLE: organization of papaya ringspot virus.
JOURNAL: J. Gen. Virol.
VOLUME: 73
PAGES: 2531-
DATE: 1992
US-08-366-490-7

Query Match 48.3%; Score 19.8; DB 2; Length 1900;
Best Local Similarity 69.2%; Pred. No. 60;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CAAAACCTAGGTCAAAGTCTATCAAACTAGGTCAAAGGT 39
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Db 1226 CAGAGCTAGGTTTAGGGCCATGAAGCTGGGGACAGGT 1264
|||

Search completed: September 11, 2004, 09:33:13
Job time : 8.447 secs

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 09:20:47 ; Search time 36.9587 Seconds
(without alignments)
5187.326 Million cell updates/sec

Title: US-09-808-388-2

Perfect score: 38

Sequence: 1 caaaactaggctcaaaaggctcaaaactaggctcaaaaggctca 38

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	38	9	US-09-808-388-2
2	26	68.4	60	10	US-09-877-705A-142
3	26	68.4	60	10	US-09-877-738A-142
4	26	68.4	60	13	US-09-947-274-142
5	26	68.4	60	17	US-10-779-595-142
6	25	65.8	41	9	US-09-808-388-3
7	25	65.8	332	9	US-09-808-388-6
8	23.6	62.1	2113	15	US-10-153-668-319
9	23.6	62.1	2886	16	US-10-264-049-778
10	22.6	62.1	2926	16	US-10-094-749-46
11	22.6	59.5	634	17	US-10-389-566-61
12	21.6	56.8	467	13	US-10-027-632-17516
13	21.6	56.8	467	16	US-10-027-632-17516
14	21.6	56.8	1161	17	US-10-437-963-27118

15	21.6	56.8	2506	13	US-10-302-172-879	Sequence 879, App
16	21.6	56.8	3051	15	US-10-198-846-11260	Sequence 11260, A
17	21.6	56.8	73634	12	US-10-052-482-121	Sequence 121, App
18	21.6	56.8	397658	9	US-09-813-320-3	Sequence 3, Appli
19	21.4	56.3	14554	9	US-09-764-860-1054	Sequence 1054, Ap
20	21.4	56.3	14554	15	US-10-074-095-1054	Sequence 1054, Ap
21	21.4	56.3	14554	16	US-10-212-872-1054	Sequence 10, Appl
22	21.4	56.3	29105	15	US-10-004-113-10	Sequence 96690, A
23	21.2	55.8	344	13	US-10-424-599-96690	Sequence 8109, Ap
24	21	55.3	511	17	US-10-021-323-8109	Sequence 13618, A
25	21	55.3	583	13	US-10-027-632-13618	Sequence 243, App
26	21	55.3	583	16	US-10-027-632-13618	Sequence 243, App
27	21	55.3	75899	9	US-09-854-883-243	Sequence 136660, A
28	21	55.3	75899	16	US-10-360-510-243	Sequence 136660, A
29	20.8	54.7	456	13	US-10-027-632-136660	Sequence 162, App
30	20.8	54.7	456	16	US-10-027-632-136660	Sequence 241240, A
31	20.8	54.7	512	13	US-09-854-867-162	Sequence 10313, A
32	20.8	54.7	598	13	US-10-027-632-241240	Sequence 10314, A
33	20.8	54.7	598	16	US-10-027-632-241240	Sequence 10313, A
34	20.8	54.7	1089	13	US-10-027-632-10313	Sequence 112, App
35	20.8	54.7	1089	13	US-10-027-632-10313	Sequence 2042, Ap
36	20.8	54.7	1089	16	US-10-027-632-10313	Sequence 15965, A
37	20.8	54.7	1089	16	US-10-027-632-10313	Sequence 14360, A
38	20.8	54.7	188794	17	US-10-027-632-10314	Sequence 211395, A
39	20.6	54.2	404	12	US-10-322-696-112	Sequence 99872, A
40	20.6	54.2	426	15	US-10-362-939-7	
41	20.6	54.2	503	17	US-10-021-323-15965	
42	20.6	54.2	529	17	US-10-021-323-14360	
43	20.6	54.2	585	13	US-10-027-632-211395	
44	20.6	54.2	585	16	US-10-027-632-211395	
45	20.6	54.2	656	13	US-10-027-632-99872	

ALIGNMENTS

RESULT 1
US-09-808-388-2
; Sequence 2, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Bereziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE element
US-09-808-388-2

Query Match 100.0%; Score 38; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.1e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAAC TAGGTC AAAGGTC AAAAGGTC AAAGGTC AAAGGTC A 38

Db 1 CAAAAC TAGGTC AAAGGTC AAAAGGTC AAAGGTC AAAGGTC A 38

Mon Sep 13 07:48:08 2004

us-09-808-388-2.sept04.rnpb

RESULT 2
US-09-877-705A-142/c
; Sequence 142, Application US/09877705A
; Publication No. US20030008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPTION
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-877-705A-142
Query Match 68.4%; Score 26; DB 10; Length 60;
Best Local Similarity 95.0%; Pred. No. 2.6;
Matches 38; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 1 CAAAAGTGGTCAAAAGGT--CAAAAGTGGTCAAAAGGTCA 38
Db 60 CAAAAGTGGTCAAAAGGTCAAAAGTGGTCAAAAGGTCA 21
RESULT 3
US-09-877-738A-142/c
; Sequence 142, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-877-738A-142
Query Match 68.4%; Score 26; DB 10; Length 60;
Best Local Similarity 95.0%; Pred. No. 2.6;
Matches 38; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 1 CAAAAGTGGTCAAAAGGT--CAAAAGTGGTCAAAAGGTCA 38
Db 60 CAAAAGTGGTCAAAAGGTCAAAAGTGGTCAAAAGGTCA 21
RESULT 4
US-09-947-274-142/c
; Sequence 142, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947,274
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877,738
; PRIOR FILING DATE: 2000-06-08
; RESULT 5
US-10-779-595-142/c
; Sequence 142, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOR
; FILE REFERENCE: 26757-702.301
; CURRENT APPLICATION NUMBER: US/10/779,595
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 09/877,243
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-10-779-595-142
Query Match 68.4%; Score 26; DB 17; Length 60;
Best Local Similarity 95.0%; Pred. No. 2.6;
Matches 38; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 1 CAAAAGTGGTCAAAAGGT--CAAAAGTGGTCAAAAGGTCA 38
Db 60 CAAAAGTGGTCAAAAGGTCAAAAGTGGTCAAAAGGTCA 21
RESULT 6
US-09-808-388-3
; Sequence 3, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14

; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE element
US-09-808-388-3

Query Match 65.8%; Score 25; DB 9; Length 41;
Best Local Similarity 92.7%; Pred. No. 5.7;
Matches 38; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 CAAAACTAGGTCAAAGG---TCAAACTAGGTCAAAGGTCA 38
|||
Db 1 CAAAACTAGGTCAAAGGTCAATCAAACTAGGTCAAAGGTCA 41
|||

RESULT 7

US-09-808-388-6
; Sequence 6, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR FILING DATE: 2000-03-14
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 332
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE/PLA2s hybrid promoter
US-09-808-388-6

Query Match 65.8%; Score 25; DB 9; Length 332;
Best Local Similarity 92.7%; Pred. No. 8.6;
Matches 38; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 CAAAACTAGGTCAAAGG---TCAAACTAGGTCAAAGGTCA 38
|||
Db 13 CAAAACTAGGTCAAAGGTCAATCAAACTAGGTCAAAGGTCA 53
|||

RESULT 8

US-10-153-668-319/c
; Sequence 319, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172

; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 319
; LENGTH: 2113
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (138)..(1583)
US-10-153-668-319

Query Match 62.1%; Score 23.6; DB 15; Length 2113;
Best Local Similarity 76.3%; Pred. No. 41;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 1764 CACATCAGCATCAAAAGGTCAACACAAAGGTCAAGGTGA 1727
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RESULT 9

US-10-264-049-778/c
; Sequence 778, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAL33P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 778
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (110)..(110)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-778

Query Match 62.1%; Score 23.6; DB 16; Length 2886;
Best Local Similarity 76.3%; Pred. No. 44;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CAAAACTAGGTCAAAGGTCAAACTAGGTCAAAGGTCA 38
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Db 926 CACATCAGCATCAAAAGGTCAACACAAAGGTCAAGGTCA 889
|||

RESULT 10

US-10-094-749-46/c
; Sequence 46, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU

QY 2 AAAC TAGTCAAAGGTC AAAACTAGGTCAAAGGTCA 38
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 298 AAAACATGTTCAAAGTCAAACCTATGTCTAACCTTA 334

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US-10-021-632-17516
, Sequence 17516, Application US/10027632
, Publication No. US20030204075A9
, GENERAL INFORMATION:
, APPLICANT: Wang, David G.
, TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
, Polymorphisms in the Human Genome
, FILE REFERENCE: 108827.129
, CURRENT APPLICATION NUMBER: US/10/027,632
, CURRENT FILING DATE: 2002-04-30
, PRIOR APPLICATION NUMBER: US 60/218,006
, PRIOR FILING DATE: 2000-07-12
, PRIOR APPLICATION NUMBER: US 60/198,676
, PRIOR FILING DATE: 2000-04-20
, PRIOR APPLICATION NUMBER: US 60/193,483
, PRIOR FILING DATE: 2000-03-29
, PRIOR APPLICATION NUMBER: US 60/185,218
, PRIOR FILING DATE: 2000-02-24
, PRIOR APPLICATION NUMBER: US 60/167,363
, PRIOR FILING DATE: 1999-11-23
, PRIOR APPLICATION NUMBER: US 60/156,358
, PRIOR FILING DATE: 1999-09-28
, PRIOR APPLICATION NUMBER: US 60/146,002
, PRIOR FILING DATE: 1999-08-09
, NUMBER OF SEQ ID NOS: 32520
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 17516
, LENGTH: 457

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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-17516

Query Match      56.8%; Score 21.6; DB 16; Length 467;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 AAAAAGTCTCAAAAGTCAAAAGTCAAAAGTCAAAAGTCA 37
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 264 AAAATTCTTCAAGTCAAAAGTCAAAAGTCAAAAGTCA 299

RESULT 14
US-10-437-963-27118/c
; Sequence 27118, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 27118
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31843C.1
US-10-437-963-27118

Query Match      56.8%; Score 21.6; DB 17; Length 1161;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 TCAAAGTCAAAAGTCAAAAGTCAAAAGTCA 38
   ||||| ||||| ||||| ||||| ||||| |||||
Db 1037 TCAAATGTCAAATCTTGGTCAATGGTCA 1010

RESULT 15
US-10-302-172-879
; Sequence 879, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids ar
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803.1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: Pf_FL_genes Version 2.0
; SEQ ID NO 879
; LENGTH: 2506
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (481)..(2154)
US-10-302-172-879

Query Match      56.8%; Score 21.6; DB 13; Length 2506;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 AAACTAGGTCAAAAGTCAAAAGTCAAAAGTCAAAAGTCA 38
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 794 AAACCAAGTCAAAAGGCGATGCTATGCTAGGTCA 829

Search completed: September 11, 2004, 14:11:09
Job time : 37.8587 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 08:16:17 ; Search time 5.97527 Seconds
(without alignments)
3529.238 Million cell updates/sec

Title: US-09-808-388-2

Perfect score: 38

Sequence: 1 caaaactaggctcaaaaggtcaaaactaggctcaaaaggtca 38

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	57.9	5910	1	US-08-135-814-1
C 2	22	57.9	5910	1	US-08-135-814-1
3	20.6	54.2	10953	4	US-08-956-171E-62
C 4	20.4	53.7	421	4	US-09-621-976-12838
5	20.4	53.7	3539	4	US-09-245-248B-59
6	20.4	53.7	3853	4	US-09-245-248B-53
7	20.4	53.7	4797	4	US-09-419-568F-25
8	20.4	53.7	4797	4	US-09-334-243B-25
9	20.2	53.2	11443	4	US-08-961-527-49
10	20	52.6	47	4	US-09-422-978-3108
11	19.8	52.1	786431	4	US-09-751-389-3
12	19.6	51.6	328	4	US-09-621-976-9939
C 13	19.6	51.6	2991	3	US-08-795-430-48
C 14	19.6	51.6	2991	4	US-09-355-700-48
15	19.6	51.6	3083	4	US-09-976-594-1022
16	19.6	51.6	66986	4	US-09-596-002-29
17	19.6	51.6	148567	4	US-09-801-876B-3
18	19.6	51.6	148567	4	US-10-254-869-3
C 19	19.6	51.6	152331	3	US-09-128-155-16
20	19.6	51.6	176373	3	US-09-128-155-17
21	19.4	51.1	321	1	US-08-322-742-11
22	19.4	51.1	478	4	US-09-023-655-1233
23	19.4	51.1	571	1	US-08-322-742-14
C 24	19.4	51.1	861	4	US-09-540-236-1011
25	19.4	51.1	2309	4	US-09-016-434-1249
26	19.4	51.1	3592	3	US-08-714-918-63
27	19.4	51.1	3592	3	US-09-265-315-63

28 19.4 51.1 3592 3 US-09-265-315-63
29 19.4 51.1 3592 3 US-09-266-417-63
30 19.4 51.1 3592 4 US-09-528-709-63
31 19.4 51.1 3592 4 US-09-527-745-63
32 19.4 51.1 6464 1 US-08-321-478-2
33 19.4 51.1 6464 1 US-08-321-478-4
34 19.4 51.1 269223 4 US-09-596-002-41
C 35 19.4 51.1 269223 4 US-09-866-108A-15751
C 36 19.4 51.1 1288 4 US-09-724-864-16
37 19.4 51.1 1288 4 US-09-724-864-16
38 19.4 51.1 1288 4 US-09-336-536-37
C 39 18.8 49.5 481 4 US-08-956-171E-730
C 40 18.8 49.5 1233 4 US-09-489-039A-2858
41 18.8 49.5 1380 4 US-09-489-039A-2858
42 18.8 49.5 2403 1 US-08-454-720A-41
43 18.8 49.5 3061 2 US-08-692-787-47
44 18.8 49.5 3061 3 US-09-097-199-47
45 18.8 49.5 3537 4 US-09-245-248B-58

ALIGNMENTS

RESULT 1

US-08-195-814-1
; Sequence 1, Application US/08195814
; Patent No. 5547869
; GENERAL INFORMATION:
; APPLICANT: DUMAS, BRUNO; Gervais, MONICA;
; APPLICANT: BERGION MAX; JOURDAN, MIREITTE; JOUSSET,
; APPLICANT: FRANCOISE XAVIERE
; TITLE OF INVENTION: NOVEL PLASMIDS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,814
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/881,054
; FILING DATE: 11-MAY-1992
; APPLICATION NUMBER: 07/278,735
; FILING DATE: 2-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1029-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5910
; TYPE: NUCLEIC ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: DENSOVIRUS
; STRAIN: DENSOVIRUS OF JUNONIA
; INDIVIDUAL ISOLATE:

Sequence 63, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 41, Appl
Sequence 15751, A
Sequence 16, Appl
Sequence 37, Appl
Sequence 730, App
Sequence 2858, Ap
Sequence 2890, Ap
Sequence 41, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 58, Appl

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/ STRANDEDNESS: UNKNOWN
/ TOPOLOGY: UNKNOWN
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: DENVOSVIRUS
/ STRAIN: DENVOSVIRUS OF JUNONIA
/ INDIVIDUAL ISOLATE:
/ DEVELOPMENTAL STAGE: LARVAE
/ HAPLOTYPE:
/ TISSUE TYPE:
/ CELL TYPE: SPODOPTERA LITTORALIS
/ CELL LINE:
/ ORGANELLE:
/ FEATURE:
/ LOCATION: 1
/ OTHER INFORMATION: N IS A OR C OR G OR T,
/ OTHER INFORMATION: WHEREIN N IS ZERO TO 50 NUCLEOTIDES IN LENGTH
/ FEATURE:
/ LOCATION: 1657
/ OTHER INFORMATION: M IS A OR C
/ FEATURE:
/ LOCATION: 5619
/ OTHER INFORMATION: Y IS C OR T
/ FEATURE:
/ LOCATION: 5910
/ OTHER INFORMATION: N IS A OR C OR G OR T,
/ OTHER INFORMATION: WHEREIN N IS ZERO TO 130 NUCLEOTIDES IN LENGTH
/ US-08-195-814-1
/
Query Match 57.9%; Score 22; DB 1; Length 5910;
Best Local Similarity 73.7%; Pred.No.12;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CAAACTAGTCAAGGTCAAAGTCAAAACTAGGTCAAAGGTCA 38
| | | | | | | | | | | | | | | | | | | | |
Db 195 CAGAAGTAGTCAAGGTCAATATAGAGGTCAAAGGTCA 158

RESULT 3
US-08-956-171E-62
; Sequence 62, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997

```

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/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mark J. Hyman
/ REGISTRATION NUMBER: 46,789
/ REFERENCE/DOCKET NUMBER: FB248P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (240) 314-1224
/ TELEFAX: (301) 309-8439
/ INFORMATION FOR SEQ ID NO: 62:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10953 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-08-956-171E-62

Query Match 54.2%; Score 20.6; DB 4; Length 10953;
Best Local Similarity 74.3%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 AAAACTAGGTCAAAGGTCAAAGTAACTAGGTCAAAGGT 36
Db 2746 AGRACAGCCCAAGATGAACCTAACACAAAGTT 2780

RESULT 4
US-09-621-976-12838/c
; Sequence 12838, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 12838
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-12838

Query Match 53.7%; Score 20.4; DB 4; Length 421;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AAAACTAGGTCAAAGGTCAAAGTAACTAGGTCA 31
Db 162 AAAACTAGGACAGAGGTCAAAATTGGTGCA 133

RESULT 5
US-09-245-248B-59
; Sequence 59, Application US/09245248B
; Patent No. 6395472
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Leary, Thomas
; APPLICANT: Erker, James
; APPLICANT: Chalmers, Michelle
; APPLICANT: Simons, John
; APPLICANT: Birkenmeyer, Larry
; APPLICANT: Muerhoff, Scott
; APPLICANT: Pilot-Matias, Tami
; APPLICANT: Desai, Suresh
; APPLICANT: Mushahwar, Isa
; TITLE OF INVENTION: METHODS OF UTILIZING THE TT VIRUS
; FILE REFERENCE: 6461.US.01
; CURRENT APPLICATION NUMBER: US/09/245,248B
; CURRENT FILING DATE: 1999-02-05
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/
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 59
/ LENGTH: 3539
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-245-248B-59

Query Match 53.7%; Score 20.4; DB 4; Length 3539;
Best Local Similarity 80.0%; Pred. No. 44;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 9 GGTCAAAGGTCAAAGTAACTAGGTCAAAGGTCA 38
Db 3462 GGTCAAAGGTCAAGCTGCTACGTCAATAGTCA 3491

RESULT 6
US-09-245-248B-53
; Sequence 53, Application US/09245248B
; Patent No. 6395472
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Leary, Thomas
; APPLICANT: Erker, James
; APPLICANT: Chalmers, Michelle
; APPLICANT: Simons, John
; APPLICANT: Birkenmeyer, Larry
; APPLICANT: Muerhoff, Scott
; APPLICANT: Pilot-Matias, Tami
; APPLICANT: Desai, Suresh
; APPLICANT: Mushahwar, Isa
; TITLE OF INVENTION: METHODS OF UTILIZING THE TT VIRUS
; FILE REFERENCE: 6461.US.01
; CURRENT APPLICATION NUMBER: US/09/245,248B
; CURRENT FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 3853
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-245-248B-53

Query Match 53.7%; Score 20.4; DB 4; Length 3853;
Best Local Similarity 80.0%; Pred. No. 44;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 9 GGTCAAAGGTCAAAGTAACTAGGTCAAAGGTCA 38
Db 3568 GGTCAAAGGTCACTGCTACGTCAATAGTGA 3597

RESULT 7
US-09-419-568P-25
; Sequence 25, Application US/09419568P
; Patent No. 6331613
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renaud, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
; TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.2
; CURRENT APPLICATION NUMBER: US/09/419,568P
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US09/354,243
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 25
; LENGTH: 4797
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-419-568F-25
Query Match 53.7%; Score 20.4; DB 4; Length 4797;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AAAACTAGTCAAAAGGTCAAACTAGGTCA 31
Db 1788 AAATCTAGTCACTGTGTAATCTAGGTCA 1817

RESULT 8
US-09-354-243B-25
; Sequence 25, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Pa
; TITLE OF INVENTION: (TIPs)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 25
; LENGTH: 4797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-354-243B-25
Query Match 53.7%; Score 20.4; DB 4; Length 4797;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AAAACTAGTCAAAAGGTCAAACTAGGTCA 31
Db 1788 AAATCTAGTCACTGTGTAATCTAGGTCA 1817

RESULT 9
US-08-961-527-49
; Sequence 49, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11443 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-49
Query Match 53.2%; Score 20.2; DB 4; Length 11443;
Best Local Similarity 75.8%; Pred. No. 66;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 AACTAGTCAAAAGGTCAAACTAGGTCAAAAGGT 36
Db 6901 AAAAGTCAAAAGTACCAAACTGATTAAGGT 6933

RESULT 10
US-09-422-978-3108
; Sequence 3108, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3108
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-23549-78 : polymorphic base G or A
US-09-422-978-3108
Query Match 52.6%; Score 20; DB 4; Length 47;
Best Local Similarity 76.7%; Pred. No. 26;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 7 TAGTCAAGGTCAAACTAGGTCAAAAGGT 36
Db 17 TAGTCCRAAGTCAAAATTAGGTAAAGAT 46

RESULT 11
US-09-751-389-3
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001067
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; CURRENT APPLICATION NUMBER: US/09/751,389
; CURRENT FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 786431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1).. (786431)
; OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Query Match 52.1%; Score 19.8; DB 4; Length 786431;
Best Local Similarity 77.4%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 AAACCTAGGTCAAAGGTCAAACCTAGGTCAA 33
Db 190533 AAAATAGGTAAAGGCGCAACCTACTTGAA 190563

RESULT 12

US-09-621-976-9939
; Sequence 9939, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9939
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9939

Query Match 51.6%; Score 19.6; DB 4; Length 328;
Best Local Similarity 73.5%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 ACTAGGTCAAAGGTCAAACCTAGGTCAAAGGTCA 38
Db 15 AGTATGACCATGGTTGAACAAGGTCAAAGGTGA 48

RESULT 13

US-08-795-430-48/c
; Sequence 48, Application US/08795430
; Patent No. 6130071
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,430
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33691
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2991 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-795-430-48

Query Match 51.6%; Score 19.6; DB 3; Length 2991;
Best Local Similarity 73.5%; Pred. No. 85;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CAAACCTAGGTCAAAGGTCAAACCTAGGTCAAAG 34
Db 1968 CAAAGTTTGAAAAGGTCACTCATGTGTGAG 1935

RESULT 14

US-09-355-700-48/c
; Sequence 48, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; Helsinki University Licensing
; Alitalo, Kari (U.S. only)
; Joukov, Vladimir (U.S. only)
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,700
FILING DATE: 05-NO. 6361946-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,430
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 01-AUG-1996
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994

ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/34140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TTLEX: 25-3856

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1 1. SEQA. SEQ ID NO: 48:
2 INFORMATION FOR SEQ ID NO: 48:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 2991 base pairs
5 TYPE: nucleic acid
6 STRANDEDNESS: single
7 TOPOLOGY: linear
8 MOLECULE TYPE: DNA (genomic)
9 SEQUENCE DESCRIPTION: SEQ ID NO: 48:
10 US-09-355-700-48

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Query Match      51.6%; Score 19.6; DB 4; Length 2991;
Best Local Similarity 73.5%; Pred. No. 85;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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1 CAAAC TAGGTCAAAGGTC AAAC T AGGTCAAAG 34
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1968 CAAAGTTTGAAAAGGTCATCAT GTGCAGAG 1935

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RESULT 15
US-09-976-594-1022
; Sequence 1022, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 1022
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 406580.1
US-09-976-594-1022

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Query Match	51.6%;	Score 19.6;	DB 4;	Length 3083;
Best Local Similarity	73.5%;	Pred. No. 86;		
Best Match	0;	Mismatches 9;	Indels 0;	Gaps 0;
25. Conservative				

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 07:30:11 : Search time 468 Seconds
(without alignments)
1881.445 Million cell updates/sec

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Perfect score: 175
Sequence: 1 cgcggcaaaactgctgaaa.....tccccagccttgctgcctcac 175

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	271	9	US-09-808-388-5
2	175	100.0	332	9	US-09-808-388-5
3	128	73.1	1080	10	US-09-865-866-17
C 4	110.8	63.3	6083	13	US-10-221-714A-440
5	94.8	54.2	6083	13	US-10-221-714A-439
6	47	26.9	3330	9	US-09-917-800A-1495
7	47	26.9	3330	12	US-10-152-319A-2157
8	47	26.9	3330	16	US-10-191-803-398
9	44.4	25.4	4990	10	US-09-865-866-97
C 10	34.2	19.5	371	15	US-10-387-495-8
C 11	32.6	18.6	54552	13	US-10-087-192-1303
12	32.4	18.5	819	13	US-10-027-632-130312
13	32.4	18.5	819	16	US-10-027-632-130312
14	32.2	18.4	573	13	US-10-027-632-50048

15	32.2	18.4	573	13	US-10-027-632-50049	Sequence 50049, A
16	32.2	18.4	573	13	US-10-027-632-50049	Sequence 69880, A
17	32.2	18.4	573	13	US-10-027-632-50049	Sequence 69881, A
18	32.2	18.4	573	13	US-10-027-632-50049	Sequence 70565, A
19	32.2	18.4	573	13	US-10-027-632-50049	Sequence 70566, A
20	32.2	18.4	573	13	US-10-027-632-50049	Sequence 70566, A
21	32.2	18.4	573	16	US-10-027-632-50048	Sequence 50048, A
22	32.2	18.4	573	16	US-10-027-632-50049	Sequence 50049, A
23	32.2	18.4	573	16	US-10-027-632-50049	Sequence 69880, A
24	32.2	18.4	573	16	US-10-027-632-50049	Sequence 69881, A
25	32.2	18.4	573	16	US-10-027-632-50049	Sequence 69881, A
26	32.2	18.4	573	16	US-10-027-632-50049	Sequence 70565, A
27	31.2	17.8	420	15	US-10-027-632-70566	Sequence 70566, A
28	31.2	17.8	1441	15	US-10-422-264-17	Sequence 17, Appl
29	31.2	17.8	2136	9	US-09-862-658-13	Sequence 13, Appl
30	31.2	17.8	2136	15	US-10-175-696-24	Sequence 24, Appl
31	31.2	17.8	2136	17	US-10-776-871-24	Sequence 24, Appl
32	31.2	17.8	2236	15	US-10-422-264-5	Sequence 5, Appl
33	31.2	17.8	2307	13	US-10-302-172-803	Sequence 23, Appl
34	31.2	17.8	2604	15	US-10-422-264-23	Sequence 1, Appl
35	31.2	17.8	2701	15	US-10-422-264-1	Sequence 1, Appl
36	31.2	17.8	3320	9	US-09-862-658-1	Sequence 22, Appl
37	31.2	17.8	3320	15	US-10-175-696-22	Sequence 22, Appl
38	31.2	17.8	3384	15	US-10-776-871-22	Sequence 29, Appl
39	30.6	17.5	250	15	US-10-422-264-29	Sequence 1474, Ap
C 40	30.6	17.5	305	9	US-09-879-536-618	Sequence 618, Ap
C 41	30.6	17.5	2856	13	US-10-231-956A-43	Sequence 43, Appl
C 42	30.6	17.5	2856	16	US-10-373-801-7	Sequence 7, Appl
C 43	30.6	17.5	2885	9	US-09-880-107-3388	Sequence 3388, Ap
C 44	30.6	17.5	2885	13	US-10-262-511-245	Sequence 245, App
C 45	30.6	17.5	2885	13	US-10-307-817-351	Sequence 351, App

ALIGNMENTS

RESULT 1

US-09-808-388-5
; Sequence 5, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment of the PLA2s promoter
US-09-808-388-5

Query Match 100.0%; Score 175; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 2.6e-54;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGCAAAACTGCTGAAATGTTTGGCATCAGTACTGACGTAGTTTCCCAA 60
Db 1 CGCGCAAAACTGCTGAAATGTTTGGCATCAGTACTGACGTAGTTTCCCAA 60

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QY 61 TCCTCAACTGTCTGCTCCAGCTGATGAGGGGAAGGAAGGATTAACCTAGGGGTATGGG 120
Db 61 TCCTCAACTGTCTGCTCCAGCTGATGAGGGGAAGGAAGGATTAACCTAGGGGTATGGG 120

QY 121 CGACCAATCCTGAGTCCACCACTGACACGCCCATCCCGACCTTGTCCTCAC 175
Db 121 CGACCAATCCTGAGTCCACCACTGACACGCCCATCCCGACCTTGTCCTCAC 175

RESULT 2
US-09-808-388-6
; Sequence 6, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; TITLE OF INVENTION: their uses
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 332
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPRE/PLA2s hybrid promoter
US-09-808-388-6

Query Match 100.0%; Score 175; DB 9; Length 332;
Best Local Similarity 100.0%; Pred. No. 2.8e-54;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 60
Db 62 CGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 121

QY 61 TCCTCAACTGTCTGCTCCAGCTGATGAGGGGAAGGAAGGATTAACCTAGGGGTATGGG 120
Db 122 TCCTCAACTGTCTGCTCCAGCTGATGAGGGGAAGGAAGGATTAACCTAGGGGTATGGG 181

QY 121 CGACCAATCCTGAGTCCACCACTGACACGCCCATCCCGACCTTGTCCTCAC 175
Db 182 CGACCAATCCTGAGTCCACCACTGACACGCCCATCCCGACCTTGTCCTCAC 236

RESULT 3
US-09-865-866-17
; Sequence 17, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 17
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-865-866-17
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Query Match 73.1%; Score 128; DB 10; Length 1080;
Best Local Similarity 89.9%; Pred. No. 1.1e-36;
Matches 160; Conservative 0; Mismatches 15; Indels 3; Gaps 2;

QY 1 CGCGCAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAA 59
Db 763 CTCGGCAAACTGCCTGAAATGTGTTTGGCATCAGGCTACTGACACGTAAGGTTTCCCAA 822

QY 60 ATCCTCAACTGTGCTCTG--CCAGCTGATGAGGGGAAGGAAGGATTAACCTAGGGGTAT 117
Db 823 ATCCTCAACTGTGCTCTGCGCCAGGCTGATGAGGGGAAGGAAGGATTAACCTAGGGGTAT 882

QY 118 GGGCGACCAATCCTGAGTCCACCACTGACACGCCCATCCCGACCTTGTCCTCAC 175
Db 883 GGGCGACCAATCCTGAGTCCACCACTGACACGCCCATCCCGACCTTGTCCTCAC 940

RESULT 4
US-10-221-714A-440/c
; Sequence 440, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 440
; LENGTH: 6083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-440

Query Match 63.3%; Score 110.8; DB 13; Length 6083;
Best Local Similarity 78.2%; Pred. No. 4.5e-30;
Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 6 CAAAACTGCCTGAAATGTGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAAATCCTC 65
Db 1324 CAAAACTACCTAAATATATATTTAACTACTACTAACACGTAATAATTTCCCAAATCCTC 1265

QY 66 AACTCTGCTGCGCAGCTGATGAGGGGAAGGAAGGATTAACCTAGGGGTATGGGGGACC 125
Db 1264 AACTCTATCTTACCACAACTAATAAAAAAATTTACCTTAAAAAATATAAACGACC 1205

QY 126 AATCTGAGTCCACCACTGACACGCCCATCCCGACCTTGTCCTCAC 175
Db 1204 AATCTAAATCCCACTAATACCAACGCCCATCCCAACCTTATACCTCAC 1155

RESULT 5
US-10-221-714A-439
; Sequence 439, Application US/10221714A
; Publication No. US20040048254A1
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GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221.714A
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: PCT/EP01/02955
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540
SEQ ID NO 439
LENGTH: 6083
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-439

Query Match 54.2%; Score 94.8; DB 13; Length 6083;
Best Local Similarity 72.4%; Pred. No. 3.8e-24;
Matches 123; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 5 GCAAACTGCTGAAATGCTTTGGCATCGCTACTCACAGTAAGTTTCCCAATCCT 64
Db 4759 GTAAATTTGTTGAATGCTTTGGTATTGTTATGATAGTAAGTTTTHAATTT 4818
Qy 65 CAACCTCTCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGCGAC 124
Db 4819 TAAATTTGTTTGTAGTTGATGAGGGGAAGAAAGGATTATTTAGGGGTATGGCGAT 4878
Qy 125 CAATCCTGAGTCCACCACTGACACGCGCCATCCCGAGCTTGCGCTCA 174
Db 4879 TAAATTTGATTTATTAATGATTACGTTTATTTTAGTTTGTGTTTA 4928

RESULT 6
US-09-917-800A-1495
Sequence 1495, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798

PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1495
LENGTH: 3330
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 X51529
US-09-917-800A-1495

Query Match 26.9%; Score 47; DB 9; Length 3330;
Best Local Similarity 60.5%; Pred. No. 1.5e-06;
Matches 95; Conservative 0; Mismatches 60; Indels 2; Gaps 1;
Qy 6 CAAAACTGCTGAAATGCTTTGGCATCGCTACTCACAGTAAGTTTCCCAATCCTC 65
Db 260 CGAAATCAGCTAAAGTTTATGATGCCACACACCCATGATGAGGGCTTTTCCGGCCCTC 319
Qy 66 AACTCTGCTGCCAGCTGATGAGGGGAAGAAAGGATTACCTAGGGGTATGGG--CGA 123
Db 320 AAGCTGTGTTGCCAGCTGTTGGGGGGAAGAAAGGGAATTAACCCAGGGCGTTGGTATGC 379
Qy 124 CCAATCCTGAGTCCACCACTGACACGCGCCATCCCC 160
Db 380 CCGTCTGTGAATCCATTATTTGGCCACACCCACCTCC 416

RESULT 7
US-10-152-319A-2157
Sequence 2157, Application US/10152319A
Publication No. US20040072160A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2157

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; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X51529
US-10-152-319A-2157

Query Match      26.9%; Score 47; DB 12; Length 3330;
Best Local Similarity 60.5%; Pred. No. 1.5e-06;
Matches 95; Conservative 0; Mismatches 60; Indels 2; Gaps 1;

QY 6 CAAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCTC 65
Db 260 CGAAATCAGCTAAAGTTTATGATGGCCACACCAATGTTATGAGGCTTTTCGGCCCTC 319

QY 66 AACTCTGTCTGCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGG--CGA 123
Db 320 AAGCTGTCTGCCAGCTGTTGGGGGAAAGGGGAAATTAACCCAGGGCGTTGGGTATGC 379

QY 124 CCAATCTGAGTCCACCACTGACCAACGCGCCATCCCC 160
Db 380 CCGTCTGTGAATCCATTATTTGGCCACACCCACTCC 416

RESULT 8
US-10-191-803-398
; Sequence 398, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 398
; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 X51529
US-10-191-803-398

Query Match      26.9%; Score 47; DB 16; Length 3330;
Best Local Similarity 60.5%; Pred. No. 1.5e-06;
Matches 95; Conservative 0; Mismatches 60; Indels 2; Gaps 1;

QY 6 CAAAACTGCTGAAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCCTC 65
Db 260 CGAAATCAGCTAAAGTTTATGATGGCCACCAATGTTATGAGGCTTTTCGGCCCTC 319

QY 66 AACTCTGTCTGCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGG--CGA 123
Db 320 AAGCTGTCTGCCAGCTGTTGGGGGAAAGGGGAAATTAACCCAGGGCGTTGGGTATGC 379

QY 124 CCAATCTGAGTCCACCACTGACCAACGCGCCATCCCC 160
Db 380 CCGTCTGTGAATCCATTATTTGGCCACACCCACTCC 416
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RESULT 9
US-09-865-866-97
; Sequence 97, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL)
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 97
; LENGTH: 4990
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2026)...(2068)
; NAME/KEY: CDS
; LOCATION: (2245)...(2389)
; NAME/KEY: CDS
; LOCATION: (2622)...(2731)
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; LOCATION: (4098)...(4240)
; US-09-865-866-97

Query Match      25.4%; Score 44.4; DB 10; Length 4990;
Best Local Similarity 61.0%; Pred. No. 1.6e-05;
Matches 72; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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QY 66 AACTCTGTCTGCCAGCTGATGAGGGGAAGAAAGGATTAACCTAGGGGTATGGGGA 123
Db 1076 AGGGCTGCCCTGCCAGCTGTGGGGAAACAAAAGGCAATGGGTATGCCCATCCGTGA 1133

RESULT 10
US-10-387-495-8/c
; Sequence 8, Application US/10387495
; Publication No. US20030162956A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Leukocyte Regulatory Factors 1 and 2
; FILE REFERENCE: PF359CI
; CURRENT APPLICATION NUMBER: US/10/387,495
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/09/603,735A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 09/055,998
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/043,483
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-387-495-8

Query Match      19.5%; Score 34.2; DB 15; Length 371;
Best Local Similarity 51.7%; Pred. No. 0.039; 73; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 23 TGTGTTGGCATCAGCTACTGACGTAAGGTTTCCCAATCCTCAACTCTGCTGCTCCAGC 82
Db 238 TGTGTTGGCAACAGCCGCCAGGCTAGGCTCCCTCAATCTCCATCCCTCCACCC 179
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Mon Sep 13 07:48:10 2004

GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50048
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50048

Query Match 18.4%; Score 32.2; DB 13; Length 573;
Best Local Similarity 53.6%; Pred. No. 0.25; Indels 0; Gaps 0;
Matches 67; Conservative

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Db	223	TGACACAGAGGGTCTTCAAGAGCAAACTCAGTCATTAGTATAGTTAGTAAGAACA	282
Qy	101	GGATTACCTAGGGGTATGGCGACCAATCCTGAGTCCACCAACTGACACGCCCATCCCC	160
Db	283	GGGGTAACAGCTGTTATGTCTCCCAAAAACAGAAATTCCTCCATCCATAATGCACAACTGC	342
Qy	161	AGCCT 165	
Db	343	AGCCT 347	

RESULT 15
US-10-027-632-50049
; Sequence 50049, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 50049
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50049

Query Match 18.4%; Score 32.2; DB 13; Length 573;
Best Local Similarity 53.6%; Pred. No. 0.25; Indels 0; Gaps 0;
Matches 67; Conservative

Qy	41	TGACAGTAAAGTTTCCCAATCCTCAACTCTGCTCCAGCTGATGAGGGGAAAG	100
Db	223	TGACACAGAGGGTCTTCAAGAGCAAACTCAGTCATTAGTATAGTTAGTAAGAACA	282
Qy	101	GGATTACCTAGGGGTATGGCGACCAATCCTGAGTCCACCAACTGACACGCCCATCCCC	160
Db	283	GGGGTAACAGCTGTTATGTCTCCCAAAAACAGAAATTCCTCCATCCATAATGCACAACTGC	342
Qy	161	AGCCT 165	
Db	343	AGCCT 347	

Search completed: September 11, 2004, 09:28:32
Job time : 469 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 09:20:47; Search time 19.3993 Seconds
(without alignments)
5187.326 Million cell updates/sec

Title: US-09-808-388-1

Perfect score: 20

Sequence: 1 caaaactagggtcaagggtca 20

Scoring table:

IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*

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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*

17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*

18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	US-09-808-388-1
2	20	100.0	20	10	US-09-877-705A-67
3	20	100.0	20	10	US-09-877-705A-68
4	20	100.0	20	10	US-09-877-738A-67
5	20	100.0	20	10	US-09-877-738A-68
6	20	100.0	20	13	US-09-947-274-67
7	20	100.0	20	13	US-09-947-274-68
8	20	100.0	20	17	US-10-779-595-67
9	20	100.0	20	17	US-10-779-595-68
10	20	100.0	38	9	US-09-808-388-2
11	20	100.0	41	9	US-09-808-388-3
12	20	100.0	52	9	US-09-808-388-4
13	20	100.0	60	10	US-09-877-705A-142
14	20	100.0	60	10	US-09-877-738A-142

C 15	20	100.0	60	13	US-09-947-274-142	Sequence 142, App
C 16	20	100.0	60	17	US-10-779-595-142	Sequence 142, App
C 17	20	100.0	332	9	US-09-808-388-6	Sequence 6, Appli
C 18	18	90.0	18	13	US-10-366-715-9	Sequence 9, Appli
C 19	17.4	87.0	118502	13	US-10-087-192-397	Sequence 397, App
C 20	17	85.0	25	14	US-10-113-877-133	Sequence 72, Appl
C 21	16.8	84.0	506	10	US-09-764-891-72	Sequence 15, Appl
C 22	16.8	84.0	506	13	US-10-091-414-15	Sequence 26314, A
C 23	16.8	84.0	2398	17	US-10-437-963-26314	Sequence 1906, Ap
C 24	16.8	84.0	74788	13	US-10-087-192-1906	Sequence 11, Appl
C 25	16.4	82.0	18	13	US-10-366-715-11	Sequence 121181,
C 26	16.4	82.0	1857	13	US-10-424-599-121181	Sequence 389, App
C 27	16.4	82.0	2286	15	US-10-153-668-389	Sequence 389, App
C 28	16.4	82.0	2473	15	US-10-153-668-383	Sequence 385, App
C 29	16.4	82.0	2473	15	US-10-153-668-385	Sequence 387, App
C 30	16.4	82.0	2572	15	US-10-153-668-387	Sequence 391, App
C 31	16.4	82.0	2584	15	US-10-153-668-391	Sequence 179, App
C 32	16.4	82.0	4292	13	US-09-925-298-179	Sequence 271, App
C 33	16.4	82.0	4292	15	US-10-102-806-179	Sequence 14617, A
C 34	16.4	82.0	5516	15	US-10-153-668-271	Sequence 14617, A
C 35	16	80.0	724	13	US-10-027-632-14617	Sequence 22, Appl
C 36	16	80.0	724	16	US-10-027-632-14617	Sequence 11556, A
C 37	15.8	79.0	31	16	US-10-238-960-22	Sequence 11556, A
C 38	15.8	79.0	659	13	US-10-027-632-11556	Sequence 271, App
C 39	15.8	79.0	659	16	US-10-027-632-11556	Sequence 13893, A
C 40	15.8	79.0	679	13	US-09-854-867-271	Sequence 9, Appli
C 41	15.8	79.0	878	15	US-10-198-846-13893	Sequence 46204, A
C 42	15.8	79.0	1269	13	US-10-210-281-11	Sequence 97508, A
C 43	15.8	79.0	1287	13	US-10-210-281-9	
C 44	15.8	79.0	1437	16	US-10-369-493-46204	
C 45	15.8	79.0	1865	13	US-10-027-632-97508	

ALIGNMENTS

RESULT 1

US-09-808-388-1

; Sequence 1, Application US/09808388

; Patent No. US20020081719A1

; GENERAL INFORMATION:

; APPLICANT: Massaad, Charbel

; APPLICANT: Berenbaum, Francis

; APPLICANT: Olivier, Jean-Luc

; APPLICANT: Salvat, Colette

; APPLICANT: Bereziat, Gilbert

; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them

; TITLE OF INVENTION: their uses

; FILE REFERENCE: ST00010

; CURRENT APPLICATION NUMBER: US/09/808,388

; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: FR/00/03262

; PRIOR FILING DATE: 2000-03-14

; PRIOR APPLICATION NUMBER: US 60/196,959

; PRIOR FILING DATE: 2000-04-13

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: PPRE element

US-09-808-388-1

Query Match 100.0%; Score 20; DB 9; Length 20;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAGGTCA 20

Db 1 CAAACTAGGTCAAGGTCA 20

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP67
US-09-877-705A-67

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
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DB 1 CAAACTAGGTCAAAGGTCA 20

RESULT 2
US-09-877-705A-67/c
; Sequence 67, Application US/09877705A
; Publication No. US2003008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPTION FACTOR ACTIVITY
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP67
US-09-877-705A-67

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
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DB 1 CAAACTAGGTCAAAGGTCA 20

RESULT 3
US-09-877-705A-68/c
; Sequence 68, Application US/09877705A
; Publication No. US2003008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPTION FACTOR ACTIVITY
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP68
US-09-877-705A-68

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
   |||||
DB 1 CAAACTAGGTCAAAGGTCA 20

RESULT 4
US-09-877-705A-67
; Sequence 67, Application US/09877705A
; Publication No. US2003008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPTION FACTOR ACTIVITY
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP67
US-09-877-705A-67

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CAAACTAGGTCAAAGGTCA 20

RESULT 5
US-09-877-738A-68/c
; Sequence 68, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP68
US-09-877-738A-68

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CAAACTAGGTCAAAGGTCA 20

RESULT 6
US-09-947-274-67
; Sequence 67, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xianqiang
; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947,274
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877,738
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,243
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,403
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,705
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:

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OTHER INFORMATION: Transcription factor probe PP67
US-09-947-274-67

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
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Db 1 CAAACTAGGTCAAAGGTCA 20

RESULT 7
US-09-947-274-68/c
; Sequence 68, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xiangqiang
; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947,274
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877,738
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,243
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,403
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,705
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP68
US-09-947-274-68

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
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Db 20 CAAACTAGGTCAAAGGTCA 1

RESULT 8
US-10-779-595-67
; Sequence 67, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xiangqiang
; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOR
; FILE REFERENCE: 26757-702.301
; CURRENT APPLICATION NUMBER: US/10/779,595
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 09/877,243
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP67
US-10-779-595-67

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAACTAGGTCAAAGGTCA 20
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Db 1 CAAACTAGGTCAAAGGTCA 20

RESULT 9
US-10-779-595-68/c
; Sequence 68, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xiangqiang
; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOR
; FILE REFERENCE: 26757-702.301
; CURRENT APPLICATION NUMBER: US/10/779,595
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 09/877,243
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP68
US-10-779-595-68

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
|||||
Db 20 CAAACTAGGTCAAAGGTCA 1

RESULT 10
US-09-808-388-2
; Sequence 2, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Bereziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PP68 element
US-09-808-388-2

Query Match 100.0%; Score 20; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
|||||

us-09-808-388-1.sept04.rnpb

Mon Sep 13 07:48:08 2004

Db 1 CAAACTAGGTCAAAGGTCA 20

RESULT 11

US-09-808-388-3
; Sequence 3, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPPE element
US-09-808-388-3

Query Match 100.0%; Score 20; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.3; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
Db 1 CAAACTAGGTCAAAGGTCA 20

RESULT 12

US-09-808-388-4
; Sequence 4, Application US/09808388
; Patent No. US20020081719A1
; GENERAL INFORMATION:
; APPLICANT: Massaad, Charbel
; APPLICANT: Berenbaum, Francis
; APPLICANT: Olivier, Jean-Luc
; APPLICANT: Salvat, Colette
; APPLICANT: Berezziat, Gilbert
; TITLE OF INVENTION: Inflammation Inducible Hybrid Promoters, Vectors Comprising them
; FILE REFERENCE: ST00010
; CURRENT APPLICATION NUMBER: US/09/808,388
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: FR/00/03262
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/196,959
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PPPE element
US-09-808-388-4

Query Match 100.0%; Score 20; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.4; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
Db 1 CAAACTAGGTCAAAGGTCA 20

RESULT 13

US-09-877-705A-142/c
; Sequence 142, Application US/09877705A
; Publication No. US20030008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-877-705A-142

Query Match 100.0%; Score 20; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.5; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
Db 60 CAAACTAGGTCAAAGGTCA 41

RESULT 14

US-09-877-738A-142/c
; Sequence 142, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-877-738A-142

Query Match 100.0%; Score 20; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.5; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 CAAACTAGGTCAAAGGTCA 20
Db 60 CAAACTAGGTCAAAGGTCA 41

RESULT 15

US-09-947-274-142/c
; Sequence 142, Application US/09947274
; Publication No. US20030017499A1
; GENERAL INFORMATION:
; APPLICANT: Li, Xiangqiang
; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS


```

; FILE REFERENCE: 26757-705
; CURRENT APPLICATION NUMBER: US/09/947,274
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 09/877,738
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,243
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,403
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/877,705
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP68
US-09-947-274-142

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Query Match      100.0%; Score 20; DB 13; Length 60;
Best Local Similarity 100.0%; Pred.No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAAAACTAGGTCAAAGGTCA 20
Db      60 CAAAACTAGGTCAAAGGTCA 41

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Search completed: September 11, 2004, 14:11:08
Job time : 20.3993 secs

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 08:16:17 ; Search time 3.14488 Seconds
(without alignments)
3529.238 Million cell updates/sec

Title: US-09-808-388-1

Perfect score: 20

Sequence: 1 caaaactaggccaagggtca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
- 2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	79.0	421	4	US-09-621-976-12838
C 2	15.4	77.0	587	3	US-09-053-702-3
C 3	15.2	76.0	3441	2	US-08-742-753-1
C 4	15.2	76.0	13865	3	US-09-009-217-11
C 5	15.2	76.0	13865	3	US-09-009-656-11
C 6	15.2	76.0	13894	1	US-08-348-891A-1
C 7	15.2	76.0	15894	1	US-08-905-817-1
C 8	15.2	76.0	580073	4	US-08-545-528D-1
C 9	15.2	75.0	2661	1	US-08-351-413-1
C 10	15.2	75.0	2661	2	US-09-025-583-1
C 11	15.2	75.0	4808	1	US-08-351-413-17
C 12	15.2	75.0	4808	2	US-09-025-583-17
C 13	14.8	74.0	328	4	US-09-621-976-9939
C 14	14.8	74.0	1140	4	US-09-328-352-1678
C 15	14.8	74.0	11303	4	US-08-961-527-115
C 16	14.8	74.0	14485	4	US-09-876-216-3
C 17	14.8	74.0	16595	4	US-09-146-053-7
C 18	14.8	74.0	118067	4	US-09-497-855A-32
C 19	14.4	72.0	480	4	US-09-134-000C-778
C 20	14.4	72.0	2372	4	US-09-620-312D-763
C 21	14.4	72.0	3127	4	US-09-620-312D-613
C 22	14.4	72.0	56804	4	US-09-740-041-3
C 23	14.4	72.0	161652	4	US-09-497-855A-40
C 24	14.4	72.0	1830121	4	US-09-557-884-1
C 25	14.4	72.0	1830121	4	US-09-643-990A-1
C 26	14.2	71.0	468	4	US-09-621-976-784
C 27	14.2	71.0	865	3	US-09-328-111-128

Sequence 3, Appli
Sequence 1308, Ap
Sequence 5681, Ap
Sequence 16, Appl
Sequence 3628, Ap
Sequence 1501, Ap
Sequence 37, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 990, App
Sequence 2, Appl
Sequence 2, Appl
Sequence 1022, Ap
Sequence 7, Appl
Sequence 48, Appl
Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-09-621-976-12838/c
; Sequence 12838, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jovert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 12838
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-12838

Query Match 79.0%; Score 15.8; DB 4; Length 421;
Best Local Similarity 89.5%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAACTAGGTCAGGTCA 20
Db 162 AAACTAGGTCAGGTCA 144

RESULT 2
US-09-053-702-3/c
; Sequence 3, Application US/09053702
; Patent No. 6229069
; GENERAL INFORMATION:
; APPLICANT: YAMADA, Shigehiro
; TITLE OF INVENTION: METHOD FOR CONTROLLING WATER CONTENT OF PLANT
; FILE REFERENCE: 230-122P
; CURRENT APPLICATION NUMBER: US/09/053,702
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-053-702-3

Query Match 77.0%; Score 15.4; DB 3; Length 587;
Best Local Similarity 94.1%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,427
; FILING DATE: 27-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,205
; FILING DATE: 27-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,920
; FILING DATE: 22-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: UTSD:537
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13865 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-009-656-11

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```

Query Match          76.0%; Score 15.2; DB 3; Length 13865;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

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Qy 1 CAAACTAGGTCAAGTGCA 20
Db 13773 CAAATTAGGTAAAGGACA 13792

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```

RESULT 6
US-08-348-891A-1/c
; Sequence 1, Application US/08348891A
; Patent No. 5654136
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Keiko
; APPLICANT: MORI, Takayuki
; APPLICANT: MAKINO, Satoshi
; TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
; TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,891A
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,400
; FILING DATE: 10-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-293625
; FILING DATE: 14-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: KB-7501

```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-521-2297
; TELEFAX: 703-685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 108..1682
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1807..3327
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3438..4442
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 5458..7107
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7271..9121
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9234..15782
; US-08-348-891A-1

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Query Match          76.0%; Score 15.2; DB 1; Length 15894;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 CAAACTAGGTCAAGTGCA 20
Db 9920 CAAACCAGTCAAGTGCA 9901

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RESULT 7
US-08-905-817-1/c
; Sequence 1, Application US/08905817
; Patent No. 5824777
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Keiko
; APPLICANT: MORI, Takayuki
; APPLICANT: MAKINO, Satoshi
; TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
; TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,817
; FILING DATE: 04-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,891
; FILING DATE: 25-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,400

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Best Local Similarity 85.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3;

QY 1 CAAAAGTGTCAAGGTCA 20
Db 21486 CAAAAGTGTCAAGGTCA 21467

RESULT 9
US-08-351-413-1
; Sequence 1, Application US/08351413
; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 20466
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; STRAIN: inbred line W-22
; PUBLICATION INFORMATION:
; AUTHORS: Hamilton et al.,
; JOURNAL: Sex Plant Reprod.
; VOLUME: 2
; PAGES: 208-
; DATE: 1989
; US-08-351-413-1

Query Match 75.0%; Score 15; DB 1; Length 2661;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 CAAAAGTGTCAAGGTCA 15
Db 21486 CAAAAGTGTCAAGGTCA 21467

FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA: JP 3-293625
APPLICATION NUMBER: 14-OCT-1991
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: KP-7501A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 108..1682
FEATURE:
NAME/KEY: CDS
LOCATION: 1807..3327
FEATURE:
NAME/KEY: CDS
LOCATION: 3438..4442
FEATURE:
NAME/KEY: CDS
LOCATION: 5458..7107
FEATURE:
NAME/KEY: CDS
LOCATION: 7271..9121
FEATURE:
NAME/KEY: CDS
LOCATION: 9234..15782
US-08-905-817-1

Query Match 76.0%; Score 15.2; DB 1; Length 15894;
Best Local Similarity 85.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3;

QY 1 CAAAAGTGTCAAGGTCA 20
Db 9920 CAAAAGTGTCAAGGTCA 9901

RESULT 8
US-08-545-528D-1/c
; Sequence 1, Application US/08545528D
; Patent No. 6537773
; GENERAL INFORMATION:
; APPLICANT: Fraser et al.
; TITLE OF INVENTION: Nucleotide sequence of the Mycoplasma Genitalium Genome, Fragment
; Patent No. 6537773
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PBI93P1
; CURRENT APPLICATION NUMBER: US/08/545,528D
; CURRENT FILING DATE: 1995-10-19
; PRIOR APPLICATION NUMBER: US 08/486,018
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/473,545
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3.1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 580073
; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
; US-08-545-528D-1

Query Match 76.0%; Score 15.2; DB 4; Length 580073;

Db 1180 CAAACTAGGTCAA 1194

```
RESULT 10
US-09-025-583-1
; Sequence 1, Application US/09025583
; Patent No. 5977433
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,583
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; APPLICATION DATA:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; STRAIN: inbred line W-22
; PUBLICATION INFORMATION:
; AUTHORS: Hamilton et al.,
; JOURNAL: Sex Plant Reprod.
; VOLUME: 2
; PAGES: 208-
; DATE: 1989
US-09-025-583-1
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Query Match 75.0%; Score 15; DB 2; Length 2661;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAA 15

Db 1180 CAAACTAGGTCAA 1194

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US-08-351-413-17/c
; Sequence 17, Application US/08351413
; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 2046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,413
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/899,072
; FILING DATE: 12-JUN-1992
; APPLICATION NUMBER: US 07/970,849
; FILING DATE: 03-NOV-1992
; APPLICATION INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-102PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4808 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: EcoRI-HindIII fragment of plasmid pTS218
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (18..401)
; OTHER INFORMATION: /label= 3'nos
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA nopaline synthase gene"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (402..737)
; OTHER INFORMATION: /label= barnase
; OTHER INFORMATION: /note= "coding region of the barnase gene of
; OTHER INFORMATION: Bacillus amyloliquefaciens"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (738..1944)
; OTHER INFORMATION: /label= PZM13
; OTHER INFORMATION: /note= "promoter region of the Zml3 gene of Zea
; OTHER INFORMATION: mays"
; FEATURE:
; NAME/KEY: -
; LOCATION: complement (1945..2281)
; OTHER INFORMATION: /label= 3'nos
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us-09-808-388-1.sept04.rni

Mon Sep 13 07:48:08 2004

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FEATURE:
NAME/KEY: - complement (2282..2554)
LOCATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: - complement (2555..3099)
LOCATION: /label= PTA29
OTHER INFORMATION: /note= "promoter region of the TA29 gene of
OTHER INFORMATION: Nicotiana tabacum"
FEATURE:
NAME/KEY: - 3100..3932
LOCATION: /label= 3583
OTHER INFORMATION: /note= "3583" promoter sequence derived from
OTHER INFORMATION: cauliflower mosaic virus isolate Cabbb-J1"
FEATURE:
NAME/KEY: - 3933..4484
LOCATION: /label= bar
OTHER INFORMATION: /note= "coding region of the phosphinothricin
OTHER INFORMATION: acetyltransferase gene"
FEATURE:
NAME/KEY: - 4485..4763
LOCATION: /label= 3'nos
OTHER INFORMATION:
FEATURE:
NAME/KEY: - 2333..2356
LOCATION: /label= BXOL2
OTHER INFORMATION: /note= "region corresponding to oligonucleotide
OTHER INFORMATION: BXOL2"
FEATURE:
NAME/KEY: - 2538..2586
LOCATION: /label= TA29SBXOL2
OTHER INFORMATION: /note= "region complementary to oligonucleotide
OTHER INFORMATION: TA29SBXOL2"
FEATURE:
NAME/KEY: - 2800..2823
LOCATION: /label= PTA29OL5
OTHER INFORMATION: /note= "region complementary to part of
OTHER INFORMATION: oligonucleotide PTA29OL5"
US-08-351-413-17
Query Match 75.0%; Score 15; DB 1; Length 4808;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAACTAGGTCAA 15
Db 984 CAAACTAGGTCAA 970
RESULT 12
US-09-025-583-17/c
Sequence 17, Application US/09025583
Patent No. 5977433
GENERAL INFORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,583
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
FILING DATE:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4808 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: ECOLI-HINDIII fragment of plasmid PTS218
FEATURE:
NAME/KEY: -
LOCATION: complement (18..401)
OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA nopaline synthase gene"
FEATURE:
NAME/KEY: -
LOCATION: complement (402..737)
OTHER INFORMATION: /label= barnase
OTHER INFORMATION: /note= "coding region of the barnase gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: -
LOCATION: complement (738..1944)
OTHER INFORMATION: /label= P2M13
OTHER INFORMATION: /note= "promoter region of the Zml3 gene of Zea
OTHER INFORMATION: mays"
FEATURE:
NAME/KEY: -
LOCATION: complement (1945..2281)
OTHER INFORMATION: /label= 3'nos
FEATURE:
NAME/KEY: -
LOCATION: complement (2282..2554)
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar gene of
OTHER INFORMATION: Bacillus amyloliquefaciens"
FEATURE:
NAME/KEY: -
LOCATION: complement (2555..3099)
OTHER INFORMATION: /label= PTA29
OTHER INFORMATION: /note= "promoter region of the TA29 gene of
OTHER INFORMATION: Nicotiana tabacum"
FEATURE:
NAME/KEY: -

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/ LOCATION: 3100...3932
/ OTHER INFORMATION: /label= 35S3
/ note= "35S3" promoter sequence derived from
/ OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-U1"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 3933...4484
/ OTHER INFORMATION: /label= bar
/ note= "coding region of the phosphinothricin
/ OTHER INFORMATION: acetyltransferase gene"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 4485...4763
/ OTHER INFORMATION: /label= 3' nos
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 2333...2356
/ OTHER INFORMATION: /label= BXOL2
/ note= "region corresponding to oligonucleotide
/ OTHER INFORMATION: BXOL2"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: complement (2538..2586)
/ OTHER INFORMATION: /label= TA29SBXOL2
/ note= "region complementary to oligonucleotide
/ OTHER INFORMATION: TA29SBXOL2"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: complement (2800..2823)
/ OTHER INFORMATION: /label= PTA29OL5
/ note= "region complementary to part of
/ OTHER INFORMATION: oligonucleotide PTA29OL5"
US-09-025-583-17

Query Match 75.0%; Score 15; DB 2; Length 4808;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAA 15
Db 984 CAAACTAGGTCAA 970
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RESULT 13
US-09-621-976-9939
/ Sequence 9939, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 9939
/ LENGTH: 328
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-621-976-9939
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Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAACCTAGGTCAAAGTCA 20
Db 31 AAACAAGGTCAAAGGTGA 48
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RESULT 14

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US-09-328-352-1678/c
/ Sequence 1678, Application US/09328352
/ Patent No. 6562958
/ GENERAL INFORMATION:
/ APPLICANT: Gary L. Breton et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
/ FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
/ CURRENT APPLICATION NUMBER: GTC99-03PA
/ CURRENT FILING DATE: 1999-06-04
/ NUMBER OF SEQ ID NOS: 8252
/ SEQ ID NO 1678
/ LENGTH: 1140
/ TYPE: DNA
/ ORGANISM: Acinetobacter baumannii
US-09-328-352-1678
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Query Match 74.0%; Score 14.8; DB 4; Length 1140;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 2 AAACCTAGGTCAAAGTTC 19
Db 986 AAAGCTTGTCAAAGGTC 969
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RESULT 15

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US-08-961-527-115/c
/ Sequence 115, Application US/08961527
/ Patent No. 6420135
/ GENERAL INFORMATION:
/ APPLICANT: Charles Kunsch
/ TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
/ NUMBER OF SEQUENCES: 391
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/961,527
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brookes, A. Anders
/ REGISTRATION NUMBER: 36,373
/ REFERENCE/DOCKET NUMBER: PB340P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 115:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11303 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
US-08-961-527-115

Query Match 74.0%; Score 14.8; DB 4; Length 11303;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAACTAGGTCAAAGGT 18
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us-09-808-388-1.sept04.rni

Mon Sep 13 07:48:08 2004

Db 7784 CAAAACAGGTCRAGGT 7767
||||| ||||| ||||| |||||

Search completed: September 11, 2004, 09:33:09
Job time : 7.14488 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 06:05:16 ; Search time 2754 Seconds
(without alignments)
1897.560 Million cell updates/sec

Title: US-09-808-388-5_COPY_1_175

Perfect score: 175
Sequence: 1 cgcgcgaactgctgaaa.....tccccagcctgtgcttcac 175

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
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26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34.8	19.9	1201	9	AL525279
2	34.4	19.7	357	14	N75549
3	33.8	19.3	368	9	AA565892
4	33.6	19.2	600	12	BG803927

C	5	33.4	19.1	507	10	BE754755
C	6	33	18.9	941	12	BM451198
C	7	32.4	18.5	474	14	T71683
C	8	32.2	18.4	723	29	CC904751
C	9	32	18.3	370	9	AI453680
C	10	32	18.3	392	9	AA405428
C	11	32	18.3	425	10	AA467514
C	12	32	18.3	449	10	BE300996
C	13	32	18.3	454	14	CB819052
C	14	32	18.3	553	10	BE237161
C	15	31.8	18.2	995	9	AL570803
C	16	31.6	18.1	422	14	CB105190
C	17	31.6	18.1	467	9	AI955727
C	18	31.6	18.1	724	12	BI822441
C	19	31.6	18.1	784	12	BI088973
C	20	31.6	18.1	1087	12	BM458295
C	21	31.4	17.9	350	10	BF394189
C	22	31.4	17.9	430	13	BY186932
C	23	31.4	17.9	810	29	EX176093
C	24	31.4	17.9	1059	28	CC271850
C	25	31.4	17.9	1141	12	BG122709
C	26	31.2	17.8	272	10	BF888447
C	27	31.2	17.8	348	9	AA701617
C	28	31.2	17.8	409	28	BZ345401
C	29	31.2	17.8	676	14	CA249326
C	30	31.2	17.8	693	14	CA172179
C	31	31.2	17.8	874	13	BU201102
C	32	31.2	17.8	910	14	CA280524
C	33	31	17.7	643	12	BG415781
C	34	31	17.7	907	29	CNS05515
C	35	31	17.7	1028	14	CB563160
C	36	31	17.7	1083	13	BQ058613
C	37	30.8	17.6	366	13	BU984495
C	38	30.8	17.6	413	12	BG829037
C	39	30.8	17.6	523	10	BG078896
C	40	30.8	17.6	629	14	CB875655
C	41	30.8	17.6	812	13	BQ229858
C	42	30.8	17.6	898	13	BU187886
C	43	30.8	17.6	925	13	BQ714058
C	44	30.8	17.6	1059	12	BM470242
C	45	30.8	17.6	1088	12	BM544574

ALIGNMENTS

RESULT 1
AL525279
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL525279 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC011YC03 3-PRIME, mRNA sequence.
1201 bp mRNA linear EST 22-MAY-2003

AL525279.2 GI:31043534
EST.
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12788772.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9221.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC011AB02NP1&cluster=9221.r. Contact :

Feng Liang Email: fliang@lifetech.com URL :

Mon Sep 13 07:48:10 2004

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DC011AB02NP1.

FEATURES

source
1. .1201
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC011VC03"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 19.9%; Score 34.8; DB 9; Length 1201;
Best Local Similarity 56.2%; Pred. No. 6.9;
Matches 63; Conservative 1; Mismatches 48; Indels 0; Gaps 0;

Qy 3 CGGCAAACTGCTGCAATGTTTGGCATCAGTACTGACACGTAAAGTTTCCCAATC 62
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Db 200 CGCCAAAATTCACATGGTGTGTAACTCCCGAGTGGGGCTAGAAATCCCATG 259
|||

Qy 63 CTCAACTCTGCTGCCAGTCTGAGGGGAGGAAAGGATTAACCTAGGGG 114
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Db 260 GTGACCTGTGACCTGCTCCCTGAGACAGGGGAGGSCAGGGAGGTCAACGKGG 311
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RESULT 2

N75549 357 bp mRNA linear EST 29-MAR-1996
LOCUS za84h02.sl Soares fetal lung NBHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:299283 3' similar to contains element LTR3 repetitive element
; mRNA sequence.

ACCESSION N75549
VERSION N75549.1 GI:1238127

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 357)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: ml3 -40 forward

High quality sequence stop: 118.

Location/Qualifiers

1. .357

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:1244207"

/db_xref="taxon:9606"

/clone="IMAGE:299283"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal lung NBHL19W"

/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer

[5'-TGTACCAATCTGAAGTGGACGGCCGCAATTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."

ORIGIN

Query Match 19.7%; Score 34.4; DB 14; Length 357;
Best Local Similarity 55.9%; Pred. No. 4.9;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 2 GCGCAAACTGCTGCAATGTTTGGCATCAGTACTGACACGTAAAGTTTCCCAAT 61
|||
Db 239 GCGCAAAATTAACAGCATGTGTGTAACTCCCGAGTGGGGTAAAGATTCCTCAT 298
|||

Qy 62 CTCAACTCTGCTGCCAGTCTGAGGGGAGGAAAGGATTAACCTAGG 112
|||

Db 299 GGTGACCTGTGACCTGCTCCCTNAGACAGGGGAGGCCAGGCANGGTCA 349
|||

RESULT 3

LOCUS AA565892 368 bp mRNA linear EST 05-SEP-1997
DEFINITION nk18hll.sl NCI CGAP Coll Homo sapiens cDNA clone IMAGE:1013925 3'
similar to contains element LTR3 repetitive element ; mRNA
sequence.

ACCESSION AA565892

VERSION AA565892.1 GI:2337531

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 368)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Elias Campo,

M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Prepared by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrip/image/image.html

Insert length: 482 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham.

Location/Qualifiers

1. .368

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1013925"

/tissue_type="tumor"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="NCI CGAP Coll"

/note="Organ: colon; Vector: Bluescript SK-; Site 1:

EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:

Oligo dT. Multiple colon tumors. 5' adaptor sequence: 5'

GAATTCGACGAG 3' 3' adaptor sequence: 5'

CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.1 kb."

ORIGIN

Query Match 19.3%; Score 33.8; DB 9; Length 368;
Best Local Similarity 58.4%; Pred. No. 7.7;
Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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QY 3 CGGCAAACTGCTGAAATGTGTTTGGCATCTACTGACAGTAAAGGTTTCCCAATC 62
D 229 CGGCAAAATAACAGCATGTGTTGTAACATCCCCCAGTGGCGGTAGGAATTTCCCATG 288
QY 63 CTCAACTCTGCTCGCCAGCTGATGAGGGGAAGGAAGGGA 103
D 289 GTGACCTGTGACCTGCTCCCTGAGACAGGGGAGGCCAGGCA 329

RESULT 4
BG803927 600 bp mRNA linear EST 20-DEC-2001
LOCUS 0243-51 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION BG803927
VERSION BG803927.1 GI:17950840
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu.X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
21671825
11812828
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
Location/Qualifiers
1..600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN
source
1..600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

Query Match 19.2%; Score 33.6; DB 12; Length 600;
Best Local Similarity 56.2%; Pred. No. 12;
Matches 63; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 63 CTCAACTCTGCTCGCCAGCTGATGAGGGGAAGGAAGGGAATACCTAGGGGTATGGCG 122
D 101 CTGAGCTCTGCTCGGAGGAGAGCGACTGGACAGAGAGCTGCTGGGGTGGCAGTG 160
QY 123 ACCAATCTGAGTCCACCACTGACACAGCCCATCCCAAGCTTGTGCTTCA 174
D 161 ACCGAGCTGAGGTCTTCTGCGGCCCGCCCGCCCGCCAGAGCCCTCTTCA 212

RESULT 5
BE754755/c 507 bp mRNA linear EST 25-APR-2001
LOCUS 208358 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE754755
VERSION BE754755.1 GI:10168747
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 507)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

QY 3 CGGCAAACTGCTGAAATGTGTTTGGCATCTACTGACAGTAAAGGTTTCCCAATC 62
D 229 CGGCAAAATAACAGCATGTGTTGTAACATCCCCCAGTGGCGGTAGGAATTTCCCATG 288
QY 63 CTCAACTCTGCTCGCCAGCTGATGAGGGGAAGGAAGGGA 103
D 289 GTGACCTGTGACCTGCTCCCTGAGACAGGGGAGGCCAGGCA 329

RESULT 4
BG803927 600 bp mRNA linear EST 20-DEC-2001
LOCUS 0243-51 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION BG803927
VERSION BG803927.1 GI:17950840
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu.X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
21671825
11812828
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
Location/Qualifiers
1..600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN
source
1..600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

Query Match 19.2%; Score 33.6; DB 12; Length 600;
Best Local Similarity 56.2%; Pred. No. 12;
Matches 63; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 63 CTCAACTCTGCTCGCCAGCTGATGAGGGGAAGGAAGGGAATACCTAGGGGTATGGCG 122
D 101 CTGAGCTCTGCTCGGAGGAGAGCGACTGGACAGAGAGCTGCTGGGGTGGCAGTG 160
QY 123 ACCAATCTGAGTCCACCACTGACACAGCCCATCCCAAGCTTGTGCTTCA 174
D 161 ACCGAGCTGAGGTCTTCTGCGGCCCGCCCGCCCGCCAGAGCCCTCTTCA 212

RESULT 5
BE754755/c 507 bp mRNA linear EST 25-APR-2001
LOCUS 208358 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE754755
VERSION BE754755.1 GI:10168747
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 507)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

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Casas, E., Wray, J.E., White, J., Cho, J., Fahrenheit, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Berlea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.960904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGAG
Plate: 55 row: 0 column: 10
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1..507
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

ORIGIN
source
1..507
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

Query Match 19.1%; Score 33.4; DB 10; Length 507;
Best Local Similarity 53.4%; Pred. No. 12;
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 43 ACAGTAAAGTTTCCCAATCTCTCTGCTGAGGAGGGAAGGAAGG 102
D 449 ACATGAAGTTTCCATCTCTTATCGGCTCCAGCACTCTGTATCGACCGCCAC 390
QY 103 ATTACCTAGGGGTATGGGAGCAACATCTGAGTCCCAACTGACCACTGACCGCCCATCCCCAG 162
D 389 ATGAATCGGTATTGCGCTTACCAGTCTTGCCGTCACAGTGGACCATCAGCTTTTCCCG 330
QY 163 CTTGTGCTC 173
D 329 ACCTGAGCCTC 319

RESULT 6
BM451198/c 941 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT_6392622 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5495177
DEFINITION 5', mRNA sequence.
ACCESSION BM451198
VERSION BM451198.1 GI:18500238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 941)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC

```

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM12121 row: k column: 18
 High quality sequence stop: 632.

FEATURES

Location/Qualifiers
 1. 941
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5495177"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 67"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.75 kb. Library constructed by Life
 Technologies."

ORIGIN

Query Match 18.9%; Score 33; DB 12; Length 941;
 Best Local Similarity 54.5%; Pred. No. 23;
 Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 54 TTCCCAATCCTCAACTCTCTCTCCAGCTGATGAGGGAAGGAGGATACCTAGG 113
 Db 716 TTCAAGATCAGGTCGCGTCTGTCAGTATGCGGAGGATGCTGGGAGCATCCCTCC 657
 QY 114 GTATGGCGACCAATCCTCAGTCCCAACTGACCAAGCCATCCCGCCAGC 163
 Db 656 ATCTGGGGANNCTTCCCAACCCACCCCTGCGGAGGATGCTGGGAGCATCCCTCC 607

RESULT 7

T71683 474 bp mRNA linear EST 01-MAR-1995
 LOCUS yc62h05.s1 StrataGene liver (#937224) Homo sapiens cDNA clone
 DEFINITION IMAGE:85305 3' similar to gb:J03048 HEMOPXIN PRECURSOR (HUMAN);
 mRNA sequence.

ACCESSION

VERSION T71683.1 GI:686204
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Hillier L., Lennon G., Becker M., Bonaldo M.F., Chiapelli B.,
 Chisoe S., Dietrich N., DuBuque T., Favello A., Gish W.,
 Hawkins M., Hultman M., Kucaba T., Lacy M., Le M., Le N.,
 Mardis E., Moore B., Morris M., Parsons J., Prange C., Rifkin L.,
 Rohlfing T., Schellenberg K., Soares M.B., Tan F., Thierry-Mieg J.,
 Trevaskis E., Underwood K., Wohlmann P., Waterston R., Wilson R.
 and Marra M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL 97044478
 MEDLINE 8889549
 PUBMED
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 511
 High quality sequence stops: 338 Source: IMAGE Consortium, LLNL This
 clone is available royalty-free through LLNL; contact the IMAGE
 Consortium (info@image.llnl.gov) for further information.
 Insert Length: 511 Std Error: 0.00
 Seq primer: -21m13

High quality sequence stop: 338.

FEATURES

Location/Qualifiers
 1. 474
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:502362"
 /db_xref="taxon:9606"
 /clone="IMAGE:85305"
 /sex="male"
 /dev_stage="49 years old"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Stratagene liver (#937224)"
 /note="Organ: liver; Vector: pBluescript SK; Site 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dr. Hepatectomy from normal male caucasian. Average
 insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor
 sequence: 5' GAATTCGGCAGAG 3' ~3' adaptor sequence: 5'
 CTCGAGTTTTTTTTTTTTTTT 3"

ORIGIN

Query Match 18.5%; Score 32.4; DB 14; Length 474;
 Best Local Similarity 53.7%; Pred. No. 25;
 Matches 66; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
 QY 31 CATCAGCTACTGACACGTAAGGTTTCCCAATCCTCAACTCTGCTCCGACGCTGATGAGG 90
 Db 296 CATGAGTTAGGCGCAAGGACCTTTCCATACACAGGCTCGGTCTTACTTNTTCATGGG 355
 QY 91 GGAAGGAAGGATTTACCTAGGGTATGGGAGCAATCCTGAGTCCACCAACTGACCCAC 150
 Db 356 CCAAGGGAAGCTCTCTCCACGTGGCTTGGGCTCTGACTTCAAGTCCAGCCACACAGCC 415
 QY 151 GCC 153
 Db 416 GCC 418

RESULT 8

CC904751 723 bp DNA linear GSS 08-AUG-2003
 LOCUS t015m08ba.r1 TAMBT Bos taurus genomic clone t015m08ba, genomic
 DEFINITION survey sequence.

ACCESSION

VERSION CC904751.1 GI:33523684
 KEYWORDS GSS.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS Lin, S., Najjar, F. Z., Adelson, D., Gill, C. A. and Roe, B. A.
 TITLE Bovine BAC End Sequences from Library TAMBT
 JOURNAL Unpublished (2003)
 COMMENT Contact: Bruce A. Roe
 Advanced Center for Genome Technology
 University of Oklahoma Department of Chemistry and Biochemistry
 620 Parrington Oval, Room 208, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Class: BAC ends
 High quality sequence stop: 367.

FEATURES

Location/Qualifiers
 1. 723
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="Angus bull T A M U Shoshone Y6 11519666"
 /db_xref="taxon:9913"
 /clone="t015m08ba"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="TAMBT"

/note="Vector: pBelOBAcl1; Site_1: HindIII; Site 2: HindIII; TAWBT Bovine BAC library (Male) produced by Texas A&M University, Department of Animal Science."

ORIGIN	Query Match	18.4%	Score 32.2;	DB 29;	Length 723;
	Best Local Similarity	56.08;	Pred. No. 36;		
	Matches	61;	Conservative	0; Mismatches 48; Indels 0; Gaps 0;	
QY	67	ACTCTGTCCTGCCAGCTGATCAGGGGGAAGAAAGGATTACCTAGGGGTATGGCGCACCA	126		
Db	569	ACCTCGCCCTGCCTCTTTACGAAGGGAACACACCCGACCAAGGCGTTTTTCCCGTCC	628		
QY	127	ATCCTGAGTCCACCACTGACCGCCATCCCGAGCCTTGTCCTCAC	175		
Db	629	ATCTTTACCCCTCCACCTCTGCTGCCTACCCAAACCTTATCCCCAC	677		

RESULT 9
AI453680
LOCUS
tj28h12.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2142897 3,
similar to contains_element PTR7 repetitive element ; , mRNA
sequence.
ACCESSION AI453680
VERSION AI453680.1
KEYWORDS GI:4283847
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 370)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgaab3-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert length: 1248 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 365.

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FEATURES
  source
    high quality sequence stop: 365.
    Location/Qualifiers
      1..370
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:2142887"
        /tissue_type="poorly differentiated adenocarcinoma with
        signet ring cell features"
        /lab_host="DH10B"
        /clone_lib="NCI CGAP Gas4"
        /note="Organ: Stomach; Vector: pCMV-SPORT6; Site 1: Salt;
        Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
        Average insert size 1.69 kb. Life Technologies catalog #:
        11549-011"

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Query Match	18.3%	Score 32	DB 9	Length 370
Best Local Similarity	55.4%	Pred. No. 29		
Matches	62	Conservative	0	Mismatches 50
			Indels	0
			Gaps	0
3	CGGCAAACTGCTGAAATGTTGTTGGCATCAGCTACTACACACGTAAGGTTTCCCAATC	62		
255	CGCCAAAATAACACAGCATGGTGTGTAAATATCCCCCGATGGGGGCTAGAAATTCGCCATG	314		

QY 63 CTCACCTCTGTCGCCAGCTGTATGAGGGGAAGAAAGGCATTACCTAGGGG 114
| | | | | | | | | | | | | | | | | | | | |
Db 315 GTGACCTGTGACCTGCTCCTTGACACAGGGAGCCAGCGAGTCAAGGGGG 366
| | | | | | | | | | | | | | | | | | | | |

RESULT 10
AA405428
LOCUS
DEFINITION
zW36A01.s1 Soares total fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:772104 3' similar to gb:U02931 TISSUE FACTOR PRECURSOR
(HUMAN), mRNA sequence.
ACCSSION
VERSION AA405428.1 GI:2062975
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy M., Le,N., Lemon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wyllie,T., Waterston,R. and Wilson,R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
Seq primer: -4lm13 fwd. ET from Amersham
High quality sequence stop: 382.
location/Qualifiers
1 . 392
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:772104"
/dev stage="8-9 weeks"
/lab host="DH10B"
/clone lib="Soares total_fetus Nb2HF8_9w"
/note="vector: pT7JD-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I oligo(dT) primer [5'
TGTTACAACCTCACTGAGGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Rento Soares and M. Estivill.

FEATURES
source

ORIGIN

Query Match	18.3%;	Score 32;	DB 9;	Length 392;
Best Local Similarity	53.1%;	Pred. No. 30;		
Matches	68;	Conservative 0;	Mismatches 60;	Indels 0; Gaps 0;
QY	11	CTGCTGAAATGTTTGGCATAGCTACTGACGTAAGGTTTCCCAATCCTCAATC	70	
Db	82	CAGACTGAAGATGCTGTGGCAGCATCTAAGGTCACCTGGCACTTTGGCCCTTCTTACCTA	141	
QY	71	TGTCCTGCACGCTGATGAGGGGAAGGAGGATACCTAGGGGTATGGCGACCAATCC	130	
Db	142	ACTGCTCTTAACGAGATCTCAAAGTACTGTTAGATGATTGCTGCGACGAGATCC	201	
QY	131	TGAGTCCA	138	
Db	202	CGGTCCA	209	

Mon Sep 13 07:48:10 2004

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE
JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 437.

FEATURES
source

1. .449
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2906865"
/tissue type="choriocarcinoma"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected by for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 18.3%; Score 32; DB 10; Length 449;
Best Local Similarity 55.4%; Pred. No. 32;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 3 CGGCAAACTGCTGAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
Db 233 CGCCAAAATACACGATGTTGTTAACTCCCCCAGTGGGGGTAGAAATCCCATG 292
QY 63 CTCACCTGCTGCTGACGATGAGGGGAGGAAAGGATTAACCTAGGG 114
Db 293 GTGACCTGTGACCTGCTGCTGACGAGGGAGCCAGGCAGTCATGTGG 344

RESULT 13

CB819052 454 bp mRNA linear EST 16-MAY-2003
EST 44 Green Apricot Fruit lambda Zap II Library Prunus armeniaca
cDNA clone ba001c13 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CB819052
CB819052.1 GI:29950859
EST.
Prunus armeniaca (apricot)
Prunus armeniaca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
1 (bases 1 to 454)
Grimplet, J., Romieu, C., Audergon, J.M., Albagnac, G., Lambert, P.,
Bouchet, J.P. and Terrier, N.
High Throughput Detection of Isogenes among 5724 3' EST from
Apricot Fruit (Prunus armeniaca)

REFERENCE
AUTHORS

Unpublished (2003)
Contact: Audergon JM
Unité de génétique et amélioration des fruits et légumes
Institut National de la Recherche Agronomique
Domaine Saint-Maurice Bp 94 84143 Montfavet cedex
Tel: 00-33-(0)4-32-72-26-68
Fax: 00-33-(0)4-32-72-26-62
Email: audergon@avignon.inra.fr
Seq primer: 17

TITLE
JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 437.

FEATURES

1. .449
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2906865"
/tissue type="choriocarcinoma"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected by for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

RESULT 11
AW467514

LOCUS
DEFINITION
he19g02.x1 NCI CGAP CML1 Homo sapiens cDNA clone IMAGE:2919506 3', similar to contains element MER31 repetitive element ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

AW467514
AW467514.1 GI:7037620
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 425)
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 421.

REFERENCE
AUTHORS
TITLE

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 421.

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 421.

FEATURES
source

1. .425
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2919506"
/tissue type="myeloid cells, 18 pooled CML cases, BCR/ABL
rearrangement positive, includes both chronic phase and
myeloid blast crisis"
/lab host="DH10B"
/clone lib="NCI CGAP CML1"
/notes="Organ: Whole Blood; Vector: pCMV-SPORT6; Site 1:
Sali; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dt. Library constructed by Life Technologies."

ORIGIN

Query Match 18.3%; Score 32; DB 10; Length 425;
Best Local Similarity 55.4%; Pred. No. 31;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 3 CGGCAAACTGCTGAATGTTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
Db 233 CGCCAAAATACACGATGTTGTTAACTCCCCCAGTGGGGGTAGAAATCCCATG 292
QY 63 CTCACCTGCTGCTGACGATGAGGGGAGGAAAGGATTAACCTAGGG 114
Db 293 GTGACCTGTGACCTGCTGCTGACGAGGGAGCCAGGCATGTCACGGTGG 344

RESULT 12
BE300996

LOCUS
DEFINITION
ba82b05.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2906865 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

BE300996
BE300996.1 GI:9184744
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
NIH-MGC http://mgc.ncbi.nlm.nih.gov/.

REFERENCE
AUTHORS

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 437.


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source
1. .454
/organism="Prunus armeniaca"
/mol_type="mRNA"
/cultivar="Bergeron"
/db_xref="taxon:36596"
/clone="ba001c13"
/dev_stage="Green stage"
/clone_lib="Green Apricot Fruit Lambda Zap II Library"
/note="Organ: Fruit; Vector: Lambda Zap II; Site 1: Eco
RI; Site 2: XhoI; Oriented library, construction described
in Molecular cloning and expression of a cDNA encoding
1-aminocyclopropane-1-carboxylate (ACC) oxidase from
apricot fruit (Prunus armeniaca cv. Bergeron) by
Mbeguile-Mbeguile D, Chahine H, Gomez RM, Gouble B, Audergon
JM, Souty M, Albagnac G, Fils-Lycaon B in Physiol Plant
105:294-303 1999"

ORIGIN
Query Match      18.3%; Score 32; DB 14; Length 454;
Best Local Similarity 65.3%; Pred. No. 32;
Matches 47; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 9 AACTGCTCCCTGAATGTTTGGCATCAGCTACTGACGAGTAAAGTTTCCCAATCCTCAAC 68
Db 358 ATCTCTCTGACAGGACTTGGCAAGAGTTTCAGAACTTCAGATTGACATTGCTCCA 299
QY 69 TCTGTCCTGCCA 80
Db 298 TCTTTCAAGCCA 287

RESULT 14
LOCUS BE237161
DEFINITION 146328 MARC 4BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001
ACCESSION BE237161
VERSION BE237161.1 GI:9021879
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 553)
Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perte, G., Holt, I., Karanycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAG
Plate: 46 row: H column: 9
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. .553
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"

ORIGIN
Query Match      18.2%; Score 31.8; DB 9; Length 995;
Best Local Similarity 56.4%; Pred. No. 57;
Matches 57; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

QY 3 CGCAAAACTGCTGAATGTTTGGCATCAGCTACTGACGTAAGTTTCCCAATC 62
Db 222 CGCAAAATACCGATGGTGGTGTAACTCCCGGAGTGGGGCTAGATTCCCATG 281
QY 63 CTCAACTCTGTCTGCCAGCTGATGAGGGGAAGGAAGGA 103

/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."

ORIGIN
Query Match      18.3%; Score 32; DB 10; Length 553;
Best Local Similarity 55.4%; Pred. No. 36;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 40 CTGACACGTAAGTTTCCCAATCCTCACTGTCTGTCGACGCTGATGAGGGAAGAAA 99
Db 130 CAGCCAAGGAGGGTGGCCCTCTCTGAGCTCTTCTGCTCCAGGCGGCGGCCCC 189
QY 100 GGGATTACTAGGGGTATGGCGACCAATCTCTGAGTCCACCAACTGACCACG 151
Db 190 AGGAGGACTGAGGGTGGGGGAGCACCTGCTGCCCTCCTGACCTGACCAGG 241

RESULT 15
LOCUS AL570803
DEFINITION AL570803 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI022YA11 3-PRIME, mRNA sequence.
ACCESSION AL570803
VERSION AL570803.2 GI:31292218
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 995)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12927470.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9221.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI022AA06NP1&cluster=9221.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI022AA06NP1.
Location/Qualifiers
1. .995
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI022YA11"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      18.2%; Score 31.8; DB 9; Length 995;
Best Local Similarity 56.4%; Pred. No. 57;
Matches 57; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

QY 3 CGCAAAACTGCTGAATGTTTGGCATCAGCTACTGACGTAAGTTTCCCAATC 62
Db 222 CGCAAAATACCGATGGTGGTGTAACTCCCGGAGTGGGGCTAGATTCCCATG 281
QY 63 CTCAACTCTGTCTGCCAGCTGATGAGGGGAAGGAAGGA 103

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us-09-808-388-5_copy_1_175.sept04.rst

Mon Sep 13 07:48:10 2004

Db 282 GTGACCTGTGACCTGTGCTCCCTGAGASAGGGAGGCCAGGSA 322

Search completed: September 11, 2004, 08:16:05
Job time : 2758 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 06:15:11 ; Search time 75 Seconds
(without alignments)
1294.885 Million cell updates/sec

Title: US-09-808-388-5_COPY_1_175
Perfect score: 175
Sequence: 1 cgcggcaaaactgctgaaa.....tccccagcctgtgctcac 175

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgm2_6/ptodata/2/ina/5B_COMB.seq.*
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5: /cgm2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgm2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.2	17.8	420	US-09-547-435-17	Sequence 17, Appl
2	31.2	17.8	1441	US-09-547-435-13	Sequence 13, Appl
3	31.2	17.8	2236	US-09-547-435-5	Sequence 5, Appl
4	31.2	17.8	2604	US-09-547-435-23	Sequence 23, Appl
5	31.2	17.8	2701	US-09-547-435-1	Sequence 1, Appl
6	31.2	17.8	3384	US-09-547-435-29	Sequence 29, Appl
C 7	30.6	17.5	305	US-09-328-111-618	Sequence 618, App
C 8	30.6	17.5	2885	US-09-016-434-1143	Sequence 1143, Ap
9	30.4	17.4	1549	US-08-856-444-1	Sequence 1, Appl
10	30.2	17.3	340	US-09-833-381-1715	Sequence 1, Appl
11	30.2	17.3	1794	US-09-620-312D-988	Sequence 988, App
12	29.2	16.7	3111	US-09-014-969-12	Sequence 12, Appl
C 13	29	16.6	204	US-09-506-729-37	Sequence 37, Appl
C 14	29	16.6	1883	US-08-202-056-2	Sequence 2, Appl
C 15	29	16.6	1933	US-08-076-093A-1	Sequence 1, Appl
C 16	29	16.6	1933	US-08-410-451-1	Sequence 1, Appl
C 17	29	16.6	1933	US-08-410-455-1	Sequence 1, Appl
C 18	29	16.6	1933	US-08-418-919-1	Sequence 1, Appl
C 19	29	16.6	1933	US-08-410-453A-2	Sequence 1, Appl
C 20	29	16.6	1933	US-08-701-265-1	Sequence 2, Appl
C 21	29	16.6	1933	US-08-410-454A-2	Sequence 1, Appl
C 22	29	16.6	1933	US-08-284-586-1	Sequence 2, Appl
C 23	29	16.6	1933	US-08-410-456A-2	Sequence 1, Appl
C 24	29	16.6	1933	US-08-805-478-1	Sequence 2, Appl
C 25	29	16.6	1933	US-08-802-627A-1	Sequence 1, Appl
C 26	29	16.6	1933	US-08-801-238-1	Sequence 1, Appl
C 27	29	16.6	1933	US-08-801-228-1	Sequence 1, Appl

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C 28      29      16.6      1933      3      US-09-104-296-1      Sequence 1, Appli
C 29      29      16.6      1933      4      US-09-023-655-1134      Sequence 1134, Ap
C 30      29      16.6      1933      5      PCT-US94-06380-1      Sequence 1, Appli
C 31      28.6      16.3      891      4      US-09-711-164-156      Sequence 156, App
C 32      28.6      16.3      3728      1      US-08-111-939-1      Sequence 1, Appli
C 33      27.6      15.8      364      4      US-09-621-976-17202      Sequence 17202, A
C 34      27.2      15.5      1662      4      US-09-543-681A-3937      Sequence 3937, Ap
C 35      27      15.4      557      4      US-09-702-705-918      Sequence 918, App
C 36      27      15.4      557      4      US-09-736-457-918      Sequence 918, App
C 37      27      15.4      557      4      US-09-614-124B-918      Sequence 918, App
C 38      27      15.4      557      4      US-09-671-325-918      Sequence 918, App
C 39      27      15.4      3021      4      US-09-556-877-182      Sequence 182, App
C 40      27      15.4      3021      4      US-09-620-412C-182      Sequence 182, App
C 41      27      15.4      3935      4      US-09-598-419-182      Sequence 182, App
C 42      27      15.4      3935      4      US-09-060-482-1      Sequence 1, Appli
C 43      26.8      15.3      1001      3      US-09-188-930-218      Sequence 218, App
C 44      26.8      15.3      1001      4      US-09-312-283C-218      Sequence 218, App
C 45      26.8      15.3      1015      3      US-09-188-930-30      Sequence 30, Appl

```

ALIGNMENTS

```

RESULT 1
US-09-547-435-17
; Sequence 17, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-17

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Query Match      17.8%      Score 31.2; DB 4; Length 420;
Best Local Similarity 55.6%      Pred. No. 0.14;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY      68      CTCTGTCTCTGCCAGCTGATGAGGGGAGGAAAGGGATTACCTAGGGGTATGGGCGACAA 127
Db      36      CTCTGCCAGACGCTGCTGTCACAGTGGGCGAGCATGACCTTTGGGGCTTGGATGCCAA 95

QY      128      TCTGTAGTCCACCACTGACCGCCCATCCCCAGCCTTGTGCTCAC 175
Db      96      TGTCCTCATCATCATGAGGAGCGCCGCCAGACCCAGACGAGGGGACAC 143

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```

RESULT 2
US-09-547-435-13
; Sequence 13, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435

```

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; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq For Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-13

Query Match
Best Local Similarity 17.8%; Score 31.2; DB 4; Length 1441;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 68 CTCCTGTCCTGCCAGCTGATGAGGGGAAGGAAAGGGATTACCTAGGGGTATGGCGACCAA 127
Db 492 CTCCTGCCACGACGCTGCTGCTCAACAGTGGCAGCATGACTTTGGGGCCTGGATGCCCAA 551

QY 128 TCCTGAGTCACCAACTGACACAGCCGCCATCCCGAGCCCTGTGCTCTAC 175
Db 552 TGTCTCATCATCATGAGGCAGGCCGCCACCCCGACCAAGGGGACCCAC 599

RESULT 3
US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-5

Query Match
Best Local Similarity 17.8%; Score 31.2; DB 4; Length 2236;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 68 CTCCTGTCCTGCCAGCTGATGAGGGGAAGGAAAGGGATTACCTAGGGGTATGGCGACCAA 127
Db 1287 CTCCTGCCACGACGCTGCTGCTCAACAGTGGCAGCATGACTTTGGGGCCTGGATGCCCAA 1346

QY 128 TCCTGAGTCACCAACTGACACAGCCGCCATCCCGAGCCCTGTGCTCTAC 175
Db 1347 TGTCTCATCATCATGAGGCAGGCCGCCACCCCGACCAAGGGGACCCAC 1394

RESULT 4
US-09-547-435-23
; Sequence 23, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435

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; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2885 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENEBANK
; CLONE: g1478280
; US-09-016-434-1143

Query Match 17.5%; Score 30.6; DB 4; Length 2885;
Best Local Similarity 56.4%; Pred. No. 0.55;
Matches 57; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 3 CGGCAAAACTGCTGAAATGTGTTGGCATCAGTACTGACACGTAAGGTTTCCCAATC 62
Db 2633 CGGCAAAATAACAGCATGTGTGTTAAATCCCCCAGTGGGGGTAGAAITCCCATG 2574
Qy 63 CTCAACTCTGCTCGCCAGCTGATGAGGGGAAGGAAGGGA 103
Db 2573 GTGACCTGTGACCTGCTCCTGAGACAGGGGAGGCCAGCA 2533

RESULT 9
US-08-856-444-1
; Sequence 1, Application US/08856444
; Patent No. 5959081
; GENERAL INFORMATION:
; APPLICANT: Lecka-Czernik, Beata
; TITLE OF INVENTION: No. 5959081el Zinc Binding LIM Protein S2-6
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT:

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DB 132 TGCTACCAACCG 146

RESULT 11
US-09-620-312D-988
; Sequence 988, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 988
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1261)
US-09-620-312D-988

Query Match 17.3%; Score 30.2; DB 4; Length 1794;
Best Local Similarity 62.7%; Pred. No. 0, 62; Indels 0; Gaps 0
Matches 47; Conservative 0; Mismatches 28; Indels 0; Gaps 0

QY 71 TGCTGTGCGAGCTGATGAGGGGAAGGAAAGGATTACTTAGGGGTATGGGGACCAATCC 130
DB 778 TGCTTGCCAGGAGGAGGGAAGCAGCAGGAAAGCCAGAGGGGGGAGAGACCCTGC 837

QY 131 TGAGTCCACCAACTG 145
DB 838 TGCTACCAACCG 852

RESULT 12
US-09-014-969-12
; Sequence 12, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

;; TITLE OF INVENTION: ENCODING THEM
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genetics Institute, Inc.
;; STREET: 87 CambridgePark Drive
;; CITY: Cambridge
;; STATE: MA
;; COUNTRY: U.S.A.
;; ZIP: 02140
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/014,969
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sprunger, Suzanne A.
;; REGISTRATION NUMBER: 41,323
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 498-8284
;; TELEFAX: (617) 876-5851
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3111 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-09-014-969-12

Query Match 16.7%; Score 29.2; DB 2; Length 3111;
Best Local Similarity 57.8%; Pred. No. 1.8;
Matches 52; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 72 GTCTGCGAGCTGATGAGGGAAGGATTACCTAGGGPATGGCGACCAATCCCT 131
Db 957 GTCTGCGGCTGATGACGAGCTTGATAGAGATACAGGTGAGCTGTCCCAATCCC 1016
QY 132 GAGTCCACCACTGACACGCCATCCCA 161
Db 1017 CATGCGGGATCTTCCACACCCGCTCTCA 1046

RESULT 13
US-09-506-729-37/c
; Sequence 37, Application US/09506729
; Patent No. 6365352
; GENERAL INFORMATION:
; APPLICANT: Yerramilli, Subrahmanyam V.
; APPLICANT: Prashar, Yatindra
; APPLICANT: Newberger, Peter
; APPLICANT: Goguen, Jon
; APPLICANT: Weissman, Sherman M.
; TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
; FILE REFERENCE: 44921-5016-US
; CURRENT APPLICATION NUMBER: US/09/506,729
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: PCT/US98/17284
; EARLIER FILING DATE: 1998-08-21
; EARLIER APPLICATION NUMBER: 60/056,844
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-506-729-37

Query Match 16.6%; Score 29; DB 4; Length 204;
Best Local Similarity 57.0%; Pred. No. 0.63;
Matches 53; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 4 GGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCC 63
Db 194 GGAACATCTGCTGCCCAATGACTGTGGTGCACATGGCTTTCTAGGATGCTGATGC 135
QY 64 TCAACTCTGCTGCCAGCTGATGAGGGAAGG 96
Db 134 TGCAGCCAGCTGGAAGCTGCAGAGGGAAGG 102

RESULT 14
US-08-202-056-2/c
; Sequence 2, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1883 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-202-056-2

Query Match 16.6%; Score 29; DB 1; Length 1883;
Best Local Similarity 57.0%; Pred. No. 1.7;
Matches 53; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 4 GGCAAACTGCTGAAATGTGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCC 63
Db 1865 GGAACATCTGCTGCCCAATGACTGTGGTGCACATGGCTTTCTAGGATGCTGATGC 1806
QY 64 TCAACTCTGCTGCCAGCTGATGAGGGAAGG 96
Db 1805 TGCAGCCAGCTGGAAGCTGCAGAGGGAAGG 1773

RESULT 15

US-08-076-093A-1/c
; Sequence 1, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human Pf4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/67211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1933 nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-076-093A-1

Query Match 16.8%; Score 29; DB 1; Length 1933;
Best Local Similarity 57.0%; Pred. No. 1.7;
Matches 53; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 4 GGCARAACTGCCTGAATGTTTGGCATCAGCTACTGACACGTAAGGTTTCCCAATCC 63
Db 1915 GGAACATCTGCTGCCAATGGACTGGTGGCTGCACATGGCTTCTAGGGATGCTGATGC 1856
QY 64 TCAACTCTGTCTGCCAGCTGATGAGGGGAAG 96
Db 1855 TGCAGCCAGCCTGGAAGCTGCAGAGGGGAAG 1823

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Job time : 76 secs